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protein search, using sw model

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April 8, 2004, 11:20:41 ; Search time 11 Seconds (without alignments)
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RESULT 1 ANX5_HUMAN PRESENTATION OF THE PRESEN ANX5 ANX5 HUMAN P08758; 01-NOV-1988 01-NOV-1988 (Rel. 09, Created) 01-NOV-1988 (Rel. 09, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha SEQUENCE FROM N.A., AND SEQUENCE. MEDLINE-88139278; PubMed=2963810; IWASAKI A., Suda M., Nakao H., Nagoya T., Saino Y., Mizoguchi T., Sato F., Yoshizaki H., Hirata M., Miy Shidara Y., Murata M., Maki M.; "Structure and expression of CDNA for an inhibitor coagulation isolated from human placenta: a new lip protein."; MEDLINE=88273202; PubMed=2968983; Pepinsky R.B., Tizard R., Mattaliano R.J., Sinclair L.K., Miller G. Browning J.L., Chow E.P., Burne C., Huang K.-S., Pratt D., Wachter Hession C., Frey A.Z., Wallner B.P.; "Five distinct calcium and phospholipid binding proteins share homology with lipocortin I."; J. Biol. Chem. 263:10799-10811(1988). "Cloning and expression of cDNA for human vascular Ca2+-dependent phospholipid-binding protein."; Eur. J. Biochem. 174:585-592(1988). "Characterization of cDNA encoding human placental protein (PP4): homology with the lipocortin family. Proc. Natl, Acad. Sci. U.S.A. 85:3708-3712(1988). SEQUENCE FROM N.A. MEDLINE=88234495; PubMed=2967495; Grundmann U., Abel K.-J., Bohn H., Loebermann H., SEQUENCE FROM N.A., AND PARTIAL S MEDLINE=88271329; PubMed=2455636; Maurer-Fogy I., Reutelingsperger Eukaryota; Metazoa; Mammalia; Eutheria; SEQUENCE FROM N.A. MEDLINE=88163463; PubMed=2964863; Funakoshi T., Hendrickson L.E., McMullen B.A., Fujii "Primary structure of human placental anticoagulant Biochemistry 26:8087-8092(1987). Stratowa C., Hauptmann R.; Kuepper H. NCBI_TaxID=9606; ANXA5 OR ANX5 OR ENX2 OR PP4. Homo sapiens (Human) EQUENCE FROM N.A. 51.5 51.1 50.2 50.2 49.8 49.8 49.5 48.5 48.1 48.1 48.1 49.1 STANDARD; Reutelingsperger C.P.M., Pieters J., Chordata; Primates; AND PARTIAL SEQUENCE ANX1_RAT ANX1_MOUSE ANX1_HORSE ANX4_FRAAN ANXD_CANFA ANXZ_BOVIN ANI2_COLLI ANI2_COLLI ANI2_COLLI ANX2_RAT ANX1_RABIT ANX2 ANXA_HUMAN ANX2 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. ALIGNMENTS McMullen B.A., Fujikawa HUMAN MOUSE ₿ Y., Arai K Miyata T., Lottspeich anticoagulant anticoagulant, of blood kawa K.; protein."; Bodo P07150 P10107 Q8hzm6 P51074 P07356 P07356 Q07936 P51662 Q29471 P04272 Q92040 7 oryctol homo sa columba homo saj equus ca rattus r mus mus bos taus mus musc rattus canis F., b Ħ

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Result

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Description

pomo

sapien

No

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ANX5_HUMAN ANX5_BOVIN ANX5_MOUSE

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ANX7 MOUSE ANX4 HUMAN ANX6 HUMAN

ANX6

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MOUSE

ANX5 CYNPY ANX4 BOVIN ANX4 PIG

P13214

cynops pyrr

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rattus gallus gall

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P48036

musculu taurus

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sapien sapien us gall

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MOUSE RAT HUMAN

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ANXB MOUSE

ANXB_RABIT
ANXB_HUMAN
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ANX8_HUMAN

149.5 148 141 131 129 124 120

ANX9_DROME

ANX3

3_HUMAN

homo sapien mus musculu

lipocortin-like

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homo sapien

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141681 segs, 52070155 residues

Scoring table: Sequence: Perfect score:

BLOSUM62

Gapop 10.0 , Gapext 0.5

US-09-787-923-2_COPY_25_72 231

RKAMKGLGTDEESILTLLTS....

ISAAFKTLFGRDLLDDLKSE

MEDLINE=88228020; PubMed=2967291;

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J. Biochem. SEQUENCE FROM

102:1261-1273(1987).

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RC TISSUEMUSEL, Ovary, and Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet Z T.E.,
RA Bownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Washin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Rillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J.,
X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)
                                                                                                                                                                                                                                                      Schlaepfer D.D., Mehlman T., Burgess W.H., Haigh "Structural and functional characterization of el calcium- and phospholipid-binding protein."; Proc. Natl. Acad. Sci. U.S.A. 84:6078-6082(1987)
                                           phospholipase A2 inhibitors from human mechanistically relevant association | J. Biol. Chem. 263:18657-18663(1988).
                                                                                  "Sedimentation equilibrium analysis of five lipocortin-related phospholipase A2 inhibitors from human placenta. Evidence agai
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Ahn N.G., Teller D.C., Bienkowski M.J.,
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gene encoding human annexin V has a TATA-less promoter with
G+C content.";
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149:253-260(1994).
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between enzyme and inhibitor.";
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Kaneko N., Ago H., Matsuda R., Inagaki E., Miyano M.;
"Crystal Structure of annexin V with its ligand K-201
channel activity inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Budisa N., Minks C., Medrano F.J., Lutz J., Huber R., Moroder L., "Residue-specific bioincorporation of non-natural, biologically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huber R., Berendes R., Burger A., Schneider M., Luecke H., Roemisch J., Paques E.-P.;
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MEDLINE=92177413; PubMed=1311770;
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"The crystal and molecular structure of human annexin V, an anticoagulant protein that binds to calcium and membranes.",
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                                                                                                                                                                                                                                                                                                                                                                                                      indirect inhibitor of the thromboplastin-specific is involved in the blood coagulation cascade. SUBUNIT: Monomer. Binds ATRX (By similarity). DOMAIN: A pair of annexin repeats may form one bin calcium and phospholipid.

SIMILARITY: Belongs to the annexin family. SIMILARITY: Contains 4 annexin repeats.

CAUTION: This protein has been independently seque
                                                                                                                                                                                                                                                                                                                                                        seven groups under different names!

DATABASE: NAME=RkD Systems' cytokine source book: Annexin 5;
WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=185".
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J03745;
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                                                                                                                                                                     ; AAB59545.1; -.; AAA35570.1; -
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15-MAR-2004 (Rel. 43, Last annotation update)
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ANXA5 OR ANX5.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (Thromboplastin inhibitor) (Anchorin CII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998
15-DEC-1998
                                                                                REPEAT
MOD RES
VARTANT
                                                                                                                                                                                                                     PIR; S27214; S27214.
                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the annexin famile: SIMILARITY: Contains 4 annexin repeats.
                                                                                                                          REPEAT
                                                                                                                                                   Annexin;
                                                                                                                                                           PROSITE;
                                                                                                                                                                                             Pfam; PF00191; annexin;
                                                                                                                                                                                                             HSSP; P08758; 1ANW
                                                                 SEQUENCE
                                                                                                          REPEAT
                                                                                                                                           Acetylation.
                                                                                                                                                                                                     InterPro; IPR001464; Annexin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                         /ARIANT
                                                                                                                                  NIT MET
                                                                                                                                                                                                                                                            FUNCTION: This protein is an anticoagulant protein the an indirect inhibitor of the thromboplastin-specific which is involved in the blood coagulation cascade. SUBUNIT: Monomer. Binds ATRX (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: RKAMKGLGTDEESILTLLITSRSNAQRQEISAAFKTLFGRDLLDDLKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                     SM00335; ANX;
                                46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE
                                                                                                                                                                            PD000143;
                                                                                                                                                                                     PR00196; ANNEXIN.
                                         Similarity
                                                                                                                                                                                                                                                                                              Biophys. Acta 1160:76-83(1992).
             RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE
                                                                                                                                                   Calcium/phospholipid-binding;
                                                                                                                                                           PS00223;
ŔĸĸĸĸĠĿĠŦĎĖĖŠĬĹŦĹĹŤŚŖŚŅĸQŖQĖĬĄVĄŖĸŤĹŖĠŖĎĹĹĎĎĹĸŚĔ
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Conservative
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23
95
179
254
254
                                 Conservative
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                                                                  AA;
                                                                                                                                                                                                                                      Belongs to the annexin family.
                                                                                                                                                            ANNEXIN; 4.
                                                                                                                                                                            Annexin; 4.
                                                                                                                                                                                                                                                                                                                                                                                                           Cetartiodactyla;
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83
155
239
314
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                                         97.0%;
95.8%;
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Pred. No. 9.2e-21
); Mismatches 0
                                                                         ANNEXIN 1.
ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
ACETYLATION
S -> T.
K -> E.
                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                           Pred.
                                                 Score 224;
                                                                   50FCE18E95F19CB0 CRC64;
                                   Mismatches
                                                                                                                                                                                                                                                                                                                                      s A.C.M., Amess B.,
Ceccarelli P., Don
                                          No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320
                                                                                                                                                                                                                                                                                                                                                                                                           Ruminantia; Pecora; Bovoidea;
                                                                                                                                                     Repeat; Blood coagulation;
                                           o,
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                                                  DB 1;
                                                                                            (BY
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                                           .5e-20
                                                                                            SIMILARITY)
                                                                                                                                                                                                                                                                                        protein that acts as
                                                                                                                                                                                                                                                                                                                          mammalian
                                                                                                                                                                                                                                                          one binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 319;
                                                                                                                                                                                                                                                                                                                  suggest distinct
                                                  Length 320
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                                                                                                                                                                                                                                                                                   complex,
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      RESULT 3
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01-FEB-1996
10-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANX5 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 31:151-157(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rodriguez-Garcia M.I., Kozak C.A., Morgan "Mouse annexin V chromosomal localization, conservation, and molecular evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96422179; PubMed=8824796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANXA5 OR ANX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Eventhe European Bioinformatics Institute. There are no restricted the surpession of the surpession of the Eventhalian of the Ev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=129/SvJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adachi
                                                                                                                                                                                                                                        EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               retrovirus.";
J. Biochem. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fernandez M.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rodriguez-Garcia M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99072820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Anchorin CII).
                      EMBL;
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EMBL;
                                                                                                                                                                                                               EMBL;
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                                                                                                                                                                                      EMBL;
                                                                                                                                                              EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: This protein is an anticoagulant protein indirect inhibitor of the thromboplastin-specific of is involved in the blood coagulation cascade. | SUBUNIT: Monomer Binds ATRX (By similarity). |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   calcium and phospholipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: A pair of annexin repeats may form
                                                                             AJ230116; CAA13092.1;
AJ230118; CAA13092.1;
AJ230120; CAA13092.1;
AJ230120; CAA13092.1;
AJ230121; CAA13092.1;
                                               AJ230121; (
AJ230122; (
                                                                                                                                                                                                                                                                    AJ230108;
AJ230110;
                                                                                                                                                                                                               AJ230111; CAA13092.1;
AJ230114; CAA13092.1;
                                                                                                                                                                                                                                                                                                                              D63423;
                                                                                                                                                                                                                                                                                                                                                       U29396;
AJ230124;
                        AJ230123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AUG-1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Belongs to the annexin family.
                                                                                                                                                                                                                                                                       CAA13092.1;
CAA13092.1;
                                                    CAA13092
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33, Last sequence up
42, Last annotation
  CAA13092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=9854034;
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co the EMBL/GenBank/DDBJ
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Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morgan R.O.,
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P14668;

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RESULT 4
ANX5_CHICK
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
  STRAIN=White leghorn; TISSUE=Liver;
MEDLINE=94215900; PubMed=8163186;
Fernandez M.P., Fernandez M.R., Morgan R.O.;
"Structure of the gene encoding anchorin CII (chick annexin V).";
                                                                               Pfaeffle M., Ruggiero F., Hofmann H., F
Yamada Y., Garrone R., von der Mark K.;
Yamado J. 9:1336-1336(1990).
                                                                                                                                       Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaeffle M., Deutzmann R., Mollenhauer J., von der Mark K.; "The structure of anchorin CII, a collagen binding protein isol from chondrocyte membrane."; J. Biol. Chem. 265:8344-8344(1990).
                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         MEDLINE=90020458; PubMed=2552626;
Moss S.E., Crumpton M.J.;
"Alternative splicing or cloning artefact?";
Trends Biochem. Sci. 14:325-325(1989).
                                                                                                            Pfaeffle
                                                                                                                                                                                                       MEDLINE=90243721; PubMed=2159478;
                                                                                                                                                                                                                         REVISIONS
                                                                                                                                                                                                                                                                                            SUGGEST SEQUENCING ERROR
                                                                                                                                                                                                                                                                                                                                Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaeffle M., Deutzmann R., Mollenhauer J., von der Mark K., "The structure of anchorin CII, a collagen binding protein isolated from chondrocyte membrane.";
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL (MEDLINE=88186917; PubMed=2833522)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
(CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
(Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANXAS OR ANXS.
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1990
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P17153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001464; Annexin. Pfam; PF00191; annexin; 4. PRINTS; PR00196; ANNEXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Anchorin CII).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calcium/phospholipid-binding; Repeat; Blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319
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ANNEXIN 2.
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Pred. No. 7
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   EMBL; U01680; AAB39917.1; —
EMBL; U01671; AAB39917.1; JOINED.
EMBL; U01672; AAB39917.1; JOINED.
EMBL; U01673; AAB39917.1; JOINED.
EMBL; U01673; AAB39917.1; JOINED.
EMBL; U01675; AAB39917.1; JOINED.
EMBL; U01676; AAB39917.1; JOINED.
EMBL; U01677; AAB39917.1; JOINED.
EMBL; U01678; AAB39917.1; JOINED.
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PTODOM; PD000143; Annexin; 4.
SMART; SM00335; ANN; 4.
PROSITE; PS00223; ANNEXIN; 4.
PROSITE; PS00223; ANNEXIN; 4.
PROSITE; PS00223; ANNEXIN; 4.
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PDB; 1ALA; 31-OCT-93.
InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bewley M.C., Boustead C.M., Walker C.M., Waller C.M., Huber "Structure of chicken annexin V at 2.25-A resolution."; Biochemistry 32:3923-3929(1993).
-!- FUNCTION: Collagen-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW
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Boustead C.M., Brown R., Walker J.H.;
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[6]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE
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SIMILARITY: Belongs to the annexin family.
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U01680; AAB39917.1;
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ANNEXIN 4.
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Matches 40; Conserv
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15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
115-MAR-2004 (Rel. 43, Last annotation update)
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (PaP-I) (PP4)
(CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
(CBP-I) (Placental anticoagulant anticoagulant-alpha) (VAC-alpha)
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                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryóta, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                     MEDLINE=93369587; PubMed=8362244;
Concha N.O., Head J.F., Kaetzel M.A., Dedman J.R., Seaton B.A.;
"Rat annexin V crystal structure: Ca(2+)-induced conformational
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANXAS OR ANXS
                                                                                                                                                                    changes.";
Science 261:1321-1324(1993).
                                                                                                                                                                                                                                                          Imai Y., Kohsaka S.;
"Structure of rat annexin V gene and
                                                                                                                                                                                                                                                                                       STRAIN=Wistar;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                    "Ca (2+)-bridging mechanism and phospholipid head the membrane-binding protein annexin V."; Nat. Struct. Biol. 2:968-974(1995).
                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                                                                                                                                                                                                                                transcripts.";
                                                                                                                                                                                                                                                                             MEDLINE=96035863; PubMed=7556178
                      MEDLINE-98272673; PubMed-9609693;
Campos B., Mo Y.D., Mealy T.R., Li C.W., Swairjo M.A., Balch C.,
Head J.F., Retzinger G., Dedman J.R., Seaton B.A.;
"Mutational and crystallographic analyses of interfacial residues
"Mutational and crystallographic analyses of interfacial residues
annexin V suggest direct interactions with phospholipid membrane
                                                                                                                   MEDLINE=96069783; PubMed=7583670;
Swairjo M.A., Concha N.O., Kaetze
                                                                                                                                      TISSUE=Kidney;
                                                                                                                                              K-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
          annexin V suggest
  Biochemistry 37:8004-8010(1998)
                                                                   -RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                     Biol. Chem. 263:10799-10811(1988).
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36, Last sequence update)
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                                                                                                                      Kaetzel M.A.,
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                                                                       OF 2-319
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                                                                                                                       Dedman J.R., Seaton B.A.;
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Ohsawa K., Imai Y., Ito D., Kohsaka S.;
"Molecular cloning and characterization of annexin
with highly hydrophilic peptide structure.";
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INTERACTION WITH DNMT1.
STRAIN=Wistar; TISSUE=Brain;
MEDLINE=96301899; PubMed=8667030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Neurochem. 67:89-97(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is involved in the blood coagulation cascade.

-!- SUBUNIT: Monomer. Binds ATRX and DNMT1.

-!- DOMAIN: A pair of annexin repeats may form one calcium and phospholipid.

-!- SIMILARITY: Belongs to the annexin family.
-!- SIMILARITY: Contains 4 annexin repeats.
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EMBL; D63337; BAA07708
EMBL; D42131; BAA07708
EMBL; D42132; BAA07708
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PDB; 2RAN; 3
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ProDom; PD000143; Annexin; 4.
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D42133; BAA07708
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13-JAN-99.
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                                                                                                                                                                                                                                           Repeat; Blood coagulation;
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  Annexin; Calcium/phospholipid-binding; Repeat.
REPEAT 26 86 ANNEXIN 1.
REPEAT 98 158 ANNEXIN 2.
REPEAT 182 242 ANNEXIN 3.
                                                                                                                                                                                  EMBL; D64134; BAA11012.1; -. HSSP; P08758; 1AVH.
InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annotor send an email to license@isb-sib.ch).
                                                                                                                      SMART; SM00335; ANX;
                                                                                                                                           PRINTS; PR00196; ANNEXIN. ProDom; PD000143; Annexin.
                                                                                                   PROSITE; PS00223;
                                                                                                                                                                                                                                                                                                                                                                                                                             between
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANX5 CYNPY
P70075;
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto T., Hikono T., Abe S.I.;
"Differential expression of annexin V during spermatogenesis in newt Cynops pyrrhogaster ",
Dev. Genes Evol. 206:64-71(1996).
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15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Annexin A5 (Annexin V).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              calcium and phospholipid.
SIMILARITY: Belongs to the annexin family.
SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis (By similarity). DOMAIN: A pair of annexin repeats may form one binding site for
                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through
sen the Swiss Institute of Bioinformatics and the EW
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                                                                                                 ANNEXIN;
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79.2%;
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ANNEXIN 2.
ANNEXIN 3.
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Pred. No. 2.9e-16;
7; Mismatches 3
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RESULT 7
ANX4_BOVIN
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or send an email to license@isb-sib.ch).
                 entities requires a license agreement
                                                                                the European Bioinformatics Institute.
                                                                                                                                                               -!- MISCELLANEOUS: Seems to bind one calcium ion with high affinity -!- SIMILARITY: Belongs to the annexin family. -!- SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                    "Structure of the trigonal crystal form of bovine annexin IV.";
Blochem. J. 329:101-106(1998).
-!- SUBUNIT: Monomer.
-!- DOMAIN: A pair of annexin repeats may form one binding site calcium and phospholipid.
                                          use by non-profit institumodified and this statement
                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                             Savoia A.,
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98070213; PubMed=9405281;
                                                                                                                                                                                                                                                                                                                                                                             Zanotti G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-1995) to the PDB data bank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sutton R.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kojima K., Yamamoto K., Irimura T., Osawa T., Ogawa H., Matsumoto 1 "Characterization of carbohydrate-binding protein p33/41: relation with annexin IV, molecular basis of the doublet forms (p33 and p41) and modulation of the carbohydrate binding activity by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL S
MEDLINE=96205957; PubMed=8631806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hamman H.C., Gaffey L.C., Lynch K.R., Creutz C.E. "Cloning and characterization of a cDNA encoding (chromobindin 4).";
                                                                                                                                                                                                                                                                                                                                                                                                                   K-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phospholipids."
J. Biol. Chem. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin (Protein II) (P12.5) (Placental anticoagulant protein II) (PAP-II)
(P4-X) (35-beta calcimedin) (Carbohydrate-binding protein P33/P41)
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 156:660-667(1988)
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MEDLINE=89050088; PubMed=2847715;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovinae; Bovinae; Bos.
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P13214;
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                                                                                                                                                                                                                                                                                                                                                                    Malpeli G., Gliubich F., Folli C.,
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323 /
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  institutions as long as its content is in no way tatement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
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Pred. No. 1.9e
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                                                                                  There are no
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Matches 34
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EMBL; D78178; BAA11243.1; -.
PIR; A31578; LUBO4.
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                                                           ANX4 PIG STANDARD; PRT; 318 AA.
1908132; Q29306;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I)
(Protein II) (P32.5) (Placental anticoagulant protein (PP4-X) (35-beta calcimedin)
                                                                                                                                                                                                                                                                              HELIX
                        NCBI_TaxID=9823;
                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                              Sus scrofa (Pig).
TIŠSUE=Intestinal epithelium;
MEDLINE=87275850; PubMed=2956093;
                                                     ANXA4 OR ANX4.
              EQUENCE.
                                                                                                                                             23
                                                                                                                                                         1 RKAMKGLGTDEESILTLLTSR$NAQRQEISAAFKTLFGRDLLDDLKSE 48
                                                                                                                                                                                                                                                                                                                                                                                                                     Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                             PS00223; ANNEXIN;
                                                                                                                                                                                Similarity
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                                                                                                                                             318
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94
178
253
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210
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182
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                                        Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                    35757 MW;
                                  Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                               74.9%;
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
L -> V (IN
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                                                                                                                                                                         Score 173; DB 1
Pred. No. 1e-13;
6; Mismatches
                                                                                                                                                                                                     86BDBDF349D774FD CRC64;
                                                                                                             318
                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; 3D-structure.
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                                                                                                                                                                                       DB 1; Length 318;
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       OC GREED DIT AC LANG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                          Winteroe A.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FISSUE=Small intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-126 FROM N.A.
                                                                                                                                                                                                                                                                             HSSP; P13214; 1ANN
     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                           23
                                                                                                          RKAMKGLGTDEDAIISVLAYRSTAQRQEIRTAYKSTIGRDLLDDLKSE 70
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Weber K., Johnsson N., Plessmann U., Van P. Vandekerckhove J.; "The amino acid sequence of protein II and
                                                                  Van P.N.,
its phosphorylation site Ca2+-modulated lipid
                                                             Soling H.-D., Ampe C
```

6:1599-1604(1987). C; the domain structure

MEDLINE=96327607; PubMed=8672129;

Evaluation and characterization of a porcine small library: analysis of 839 clones."; Fredholm M., Davies W.;

intestine cDNA

-i- FUNCTION: Calcium/phospholipid-binding protein membrane fusion and is involved in exocytosis Genome 7:509-517(1996) 1 which (By sim ich promotes similarity).

-!- SUBUNIT: Monomer.
-!- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
-!- MISCELLANEOUS: Seems to bind one calcium ion with high affinity
-!- SIMILARITY: Belongs to the annexin family.
-!- SIMILARITY: Contains 4 annexin repeats.

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Pfam; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 4. EMBL; F14682; CAA23194.1; PIR; A27107; LUPG4. PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation; InterPro; IPR001464; Annexin

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μ.	Query Match Best Local S Matches 34	REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT MOD_RES MOD_RES SEQUENCE
RKAMKGLGTI	74. 11 Similarity 70. 34; Conservative	22 94 178 253 1 6 318 AA;
DEESILTLLT	74.5%; 70.8%; 7ative	313 154 313 313 313 313
RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 40	Query Match 74.5%; Score 172; DB 1; Length 318; Best Local Similarity 70.8%; Pred. No. 1.3e-13; Matches 34; Conservative 7; Mismatches 7; Indels	22 82 ANNEXIN 1. 24 154 ANNEXIN 2. 25 313 ANNEXIN 4. 25 313 ACETYLATION (BY PKC). 26 6 PHOSPHORYLATION (BY PKC). 318 AA; 35697 MW, FATD9CE2B7C631E8 CRC64;
\FKTLFGRDLL : :	DB 1; Length 3 3e-13; Indels	(PROBABLE) TON (BY PK
DDLKSE 48	gth 318; ndels	64:

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Euteleostomi;

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Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;
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ProDom; PD000143; Annexin; 8.
SMART; SM00335; ANX; 8.
                                                                                                                                                                                                                                                                                                                                                               PDB; 1AVC; 28-JAN-98.
InterPro; IPR001464; Annexin.
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U87539; AAB47570.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).

-!- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
-!- SIMILARITY: Belongs to the annexin family.
-!- SIMILARITY: Contains 8 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 1387:103-116(1998).

-- FUNCTION: May associate with CD21. May regulate the release of Ca(2+) from intracellular stores.

--- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.

--- PTM: Phosphorylated in response to growth factor stimulation (By
                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00191; annexin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98422308; PubMed=9748523;
Avila-Sakar A.J., Creutz C.E., Kretsinger R.H.,
"Crystal structure of bovine annexin VI in a calcium-bound state.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Comera C., Creutz C.E.;
Submitted (JAN-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE≂Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                119
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                                                  -!- FUNCTION: Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis.
-!- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
-!- SIMILARITY: Belongs to the annexin family.
-!- SIMILARITY; Contains 4 annexin repeats.
                                                                                                            comparison with other synexins.";
Biochem. J. 289:735-741(1993).
                                                                                                                           MEDLINE=93168121; PubMed=7916616;
Zhang-Keck Z.Y., Burns A.L., Pollard H.B.;
"Mouse synexin (annexin VII) polymorphisms and a phylogenetic
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                              ANXA7 OR ANX7.
                                                                                                                                                                                                                      01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Annexin A7 (Annexin VII) (Synexin).
                                                                                                                                                                                                                                                                     ANX7
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                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                   MOUSE
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                                                                                                                                                                                                                                                                                                                                                  33;
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358
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                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                 69796 MW;
                                                                                                                                                                                                                                                                                                                                                        73.6%; Score 170; 68.8%; Pred. No. 4
                                                                                                                                                                                                                     (Synexin)
                                                                                                                                                                                                                                                                                                                                                                                  5571F70F24B5836F CRC64;
                                                                                                                                                                                                                                                                                                                                                Mismatches
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        There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                         4.6e-13;
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                            and the EMBL outstation
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                                   a collaboration
  for commercial
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Best Local (
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P09525; 096F3; Q9BWK1;

01-MAR-1989 (Rel. 10, Created)

01-OCT-1996 (Rel. 34, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

10-OCT-2003 (Rel. 42, Last annotation update)

Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chrc
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin II) (P32.5) (Placental anticoagulant protein II) (PP4-X) (35-beta calcimedin) (Carbohydrate-binding protein
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Pfam; PF00191; annexin; 4.
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                          ANXA4 OR ANX4
                    "Characterization of human p33/41 (annexin IV), a Ca2+ deg carbohydrate-binding protein with monoclonal anti-annexin antibodies, AS11 and AS17.";
                                                                                                                                                                                                          Grundmann U., Amann E., Abel K.-J., Kuepp
"Isolation and expression of cDNA coding
phospholipase A2 inhibitor family.";
                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                              SEQUENCE FROM N.A. MEDLINE=97239215; PubMed=9084877;
                                                                                                                                      Tait J.F.,
Disteche C.
                                                                                                              "Chromosomal mapping of t
Genomics 12:313-318(1992)
                                                                                                                                                           MEDLINE=92155721;
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                              Behring
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                                                         Matsumoto
                                                                    Satoh A.,
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
            Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 48
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                                                                   Takayama
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64.6%;
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                                                                                                                                                    Frankenberry
                                                                      Kojima K.,
                                                                                                                              the human
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ANNEXIN 4.
3 X 5 AA T/
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Pred. No. 4.5e-13;
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                                                                                                                                                    D.A., Miao C.H., Adler D.A.,
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                                                                      Ogawa H., Katsura Y.,
                                                                                                                            annexin
                                                                                                                                                                                                                                   Kuepper H.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    318
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                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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                                                                                                                                                                                                                        for a new
                                                                                                                               IV (ANX4) gene.";
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n P33/P41)
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A Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

A Hopkins R.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Wullahy S.J.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R. D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.:
Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-len human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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MEDLINE=89118212; PubMed=2975506;
Tait J.F., Sakata M., McMullen B.A., Miao C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sedimentation equilibrium analysis of five lipocortin-related phospholipase A2 inhibitors from human placenta. Evidence against mechanistically relevant association between enzyme, and inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Eye,
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Abn N.G., Teller D.C., Bienkowski
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                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human placental annexin IV."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91073383; PubMed=2254922; Freemont P.S., Driessen H.P.C., Verbi W., Crumpton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             placental anticoagulant proteins: isolation and comparative characterization four members of the lipocortin family.";
                                                                                                    EMBL; M1938; AAC41689 1; ALT_INIT-
EMBL; M82809; AAAS1740.1; -.
EMBL; D78152; BAA11227.1; ALT INIT-
EMBL; BC000182; AAH00182.1; ALT_INI
EMBL; BC011659; AAH11659.1; ALT_INI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Crystallization and preliminary X-ray crystallographic
                      HSSP; P13214; IANN
SWISS-2DPAGE; P09525; HUMAN
PMMA-2DPAGE; P09525; -
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                                                              PIR; A42077; A42077.
HSSP; P13214; 1ANN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iochemistry 27:6268-6276(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wol. Biol. 216:219-221(1990).
FUNCTION: Calcium/phospholipid-binding protein membrane fusion and is involved in exceptosis
                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               calcium and phospholipid.
MISCELLANEOUS: Seems to bind one calcium ion
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the annexin tamily.
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e binding site for
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         SEQUENCE FROM N.A.
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MEDLINE=89380132; PubMed=2528541;
Iwasaki A., Suda M., Watanabe M.,
Saino Y., Shidara Y., Maki M.;
                                         "Structure and
protein from h
                                                                      Yoshizaki H.,
                                                                                  MEDLINE=90236978; PubMed=2139657;
                                                                                               SEQUENCE
                                                                                                                                 placental
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01-APR-1990 (Rel. 14, Last sequence update)
15-MAR-2004 (Rel. 15, Last annotation update)
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB ANXA6 OR ANXA6.
                                                                                                                                                                                                            Proc. Natl. Acad.
                                                                                                                                                                                                                                       Suedhof T.C., Slaughter C.A., Leznicki I.,
                                                                                                                                                                                                                                                                                     "Primary structure of the human, membrane-associated Ca2+-binding protein p68 a novel member of a protein family."; EMBO J. 7:21-27(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANX6_HUMAN
P08133;
                                                                                                                Structure and expression of cDNA for calphobindin lacental coagulation inhibitor.";
J. Biochem. 106:43-49(1989).
                                                                                                                                                                                                      "Human 67-kDa caleTectrin contains a duplication found in 35-kDa lipocortins."; Proc. Natl. Acad. Sci. U.S.A. 85:664-668(1988).
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                                                                                                                                                                                                                                                                                                                                         MEDLINE=88196081; PubMed=3258820;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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CONFLICT
SEQUENCE
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INIT_MET
REPEAT
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InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
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                               Biochem.
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                              m human placenta.";
107:43-50(1990).
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                                                                    Mizoguchi T.,
                                              properties of calphobindin II, an anticoagulant
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Pred. No. 5.4e-13;
9; Mismatches 7
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ANNEXIN 2.
ANNEXIN 3.
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                                                                  Shiratsuchi M., Shidara Y.,
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Hopkins R.F., Jordan R.C., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Mcorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Mcorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
Proc. Mart P. Danad Scit if C. a. a. 1.000 full-length
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PRINTS; PR00196; ANNEXIN.
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EMBL; Y00097; CAA68286.1; -.
EMBL; J03578; AAA35656.1; -.
EMBL; BC017046; AAH17046.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- DOMAIN: A pair of annexin repeats may form calcium and phospholipid.
-i- PTM: Phosphorylated in response to growth
-i- MISCELLANEOUS: Seems to bind one calcium i.
-i- SIMILARITY: Belongs to the annexin family.
-i- SIMILARITY: Contains 8 annexin repeats.
                                                                                                                                   REPEAT
                                                                                                                                                 Phosphorylation;
INIT MET 0
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J. Mol. Biol. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The structure of recombinant human
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FUNCTION: May associate with CD21. May regulate the release Ca(2+) from intracellular stores.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation UPdate)
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)
(Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANX6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cao X., Genge B.R., Wu L.N., Buzzi W.R., Showman "Characterization, cloning and expression of the chicken growth plate cartilage matrix vesicles.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P51901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                     REPEAT
REPEAT
                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; S67466; AAB29337.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANXA6 OR ANX6.
                                                                                                                                                                                                                                                                                                                   ProDom; PD00014
SMART; SM00335;
                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P79134; 1AVC.
InterPro; IPR001464; Annexin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; JC2029; JC2029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94092130; PubMed=8267590;
                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 8.
                                                                                           REPEAT
                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                     Annexin;
                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00191; annexin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: A pair of annexin repeats may form calcium and phospholipid.
SIMILARITY: Belongs to the annexin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 8 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: May associate with CD21. May regulate the release Ca(2+) from intracellular stores (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE
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Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             requires a license agreement
                                                                                                                                                                                                                                                                                            PS00223; ANNEXIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biophys. Res.
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71.9%;
70.8%;
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                                                                                                                ANNEXIN 1.
ANNEXIN 2.
ANNEXIN 3.
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ANNEXIN 5.
ANNEXIN 6.
ANNEXIN 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 167;
Pred. No. 1.
      Pred.
                         Score
                                                                                           ANNEXIN
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                                                                         D0E02F4311A93D98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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D (IN REF. 1).
      No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.
                                                                                                                                                                                                                                                                       Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2e-12;
                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ere are no restrictions as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage by and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2)
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                         Length 671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.M., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wuthier R.E.; A annexin from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANX4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Annexin A4 (Annexin IV) (15pocortin IV) (36 k
membrane associated protein) (ZAP36).
                                                                  CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          granule membrane associated protein, in ex
Biochim. Biophys. Acta 1575:148-152(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fukuoka S.-I., Horst N., Nazuma - T. an annexin-like, 2 "Cloning and characterization of ZAP36, an annexin-like, 2 "Cloning and characterization of TAP36, an annexin-like, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE STRAIN-Mongrel; TISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Čhordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P50994;
01-OCT-1996
                                                                                                                     REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the regulated exocytosis of the pancreas.",
Biosci. Biotechnol. Biochem. 58:1282-1285 (1994).
-i- FUNCTION: Calcium/phospholipid-binding protein
membrane fusion and is involved in exocytosis (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Mongrel; TISSUE=Pancreas; MEDLINE=22015264; PubMed=12020832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANXA4 OR ANX4.
                                                                                                                                                        REPEAT
                                                                                                                                                                                                                             ProDom; PD000143; Annexin; 4. SMART; SM00335; ANX; 4.
                                                                                                                                                                                                                                                                                                                     EMBL; D38223; BAA07398.1;
HSSP; P13214; 1ANN.
                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- DOMAIN: A pair of annexin repeats may form one
calcium and phospholipid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukuoka S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94362286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9615;
                                                                                                                                                                                           Annexin;
                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                  PRINTS; PR00196; ANNEXIN.
                                                                                                                                                                                                                                                                                   Pfam; PF00191; annexin;
                                                                                                                                                                                                                                                                                                 InterPro; IPR001464; Annexin.
                                                                                                      REPEAT
                                                                                                                                                                            INIT MET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the annexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (By similarity)
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                                                                                                                                                                                           Calcium/phospholipid-binding;
                                                                                                                                                                                                             PS00223; ANNEXIN; 4.
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                                                                                                    82
154
238
313
                                                                                                                                                                                                                                                                                                                                                                                             license agreement
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                                                                   35681
                                                                   MW;
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                                                                                                   ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
Score 165; DB 1; I
Pred. No. 9.5e-13;
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                                                                                                                                                        ANNEXIN
                                                                     42EF5B89179B4863
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                                                                                        (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318
                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/ann
                                                                                                                                                                                            Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family.
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                                                                     CRC64;
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                                                                                        SEQUENCE)
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Canis.
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Query Match Best Local S Matches 31

Similarity

71.4%; 64.6%;

Length

Indels

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Gaps

Conservative

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23

RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 48

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() Db
                                                                                                                                                                                      RESULT 15
ANX6_MOUSE
                                                              Best Local Similarity Matches 32; Conserv
                                                                                        Query Match
                                                                                                                               REPEAT
REPEAT
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REPEAT
                                                                                                                                                                                                                                           Annexin;
INIT_MET
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REPEAT
                                                                                                                                                                                                                                                                                 PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 8.
SMART; SM00335; ANX; 8.
                                                                                                                                                                                                                                                                                                                                                                             EMBL; X13460; CAA31808.1; -. PIR; S01786; S01786.
                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calcium and phospholipid.
-!- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
-!- SIMILARITY: Belongs to the annexin family.
-!- SIMILARITY: Contains 8 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)
(Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- DOMAIN: A pair of annexin repeats may form one binding site for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89030687; PubMed=2972541;
MOSS S.E., Crompton M.R., Crumpton M.J.;
"Molecular cloning of murine p68, a Ca2+-binding protein of the lipocortin family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P14824;
01-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eur. J. Biochem. 177:21-27(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/c;
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                                                                                                                                                                                                                                                                     ROSITE;
                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:88255; Anxa6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                        fam; PF00191; annexin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANXA6 OR ANX6.
                                                                                                                                                                                                                                                                                                                                                                P79134; 1AVC
                                                           32;
     RKAMKGIGTDEATIIDIVTHRSNAQRQQIRQTFKSHFGRDLMADLKSE 419
                    RKAMKGLGTDEESIITLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 48
                                                                                                                                                                                                                                                          Calc:
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                                                                                                                                                                                                                                                                                                                                     IPR001464; Annexin
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                                                                                                                  672 AA;
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                                                                                                                  75755 MW;
                                                                         71.0%;
66.7%;
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
ANNEXIN 6.
ANNEXIN 7.
ANNEXIN 7.
                                                           Score 164; DB 1; Length 672;
Pred. No. 2.7e-12;
8; Mismatches 8; Indels
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                                                                                                                                                                                                                                                       Repeat
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Search completed: April 8, 2004, 11:57:13
Job time: 11 secs

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- 2004	version
Compugen	5.1.6
Ltd.	,

Run on: Searched: OM protein -Total number of hits satisfying chosen parameters: Scoring table: Sequence: Perfect score: Title: protein search, using sw model US-09-787-923-2_COPY_25_72 231 April BLOSUM62 Gapop 10.0 , 1586107 seqs, 282547505 residues RKAMKGLGTDEESILTLLTS.....ISAAFKTLFGRDLLDDLKSE 8, 2004, 11:18:15; Search time 55 Seconds (without alignments) Gapext 0.5 246.587 Million cell updates/sec 1586107 48

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database A_Geneseq_29Jan04:* l: geneseqp1980s:* geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:* geneseqp2000s:* geneseqp1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

Result

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Aay92930	Aar13083	Aab50863	Aabbudbb	AQUUO CA	700000000000000000000000000000000000000	2001220	Aav84788	Aay13923	Aar11910	Aar13082	Aap91953	Афитос	Mapacooo	2000000	222000111	3 a 5 0 5 1 1	Aug 2017	34056187	20055088	2000000	Mar41021	242C180	2000000	2002464	72507	Abu00010	Description
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Human Human

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Human Modif

Rat ar Rat Pi

Ade56185

Rat Pr

Abg74925 Abg74924

Chicke Chicke Mouse Aap80714

Sequen CPB-1

S65T 0

Aar25718

ALIGNMENTS

RESULT 1 ABU00010 ABU00010 standard; protein; 117 AA. Human novel polypeptide #103. ABU00010; 17-JAN-2003 (first entry)

osteoarthritis; periodontal disease; liver fibrosis; viral infection fungal infection; bacterial infection; autoimmune disease; diabetes, neurodegenerative disorder; lymphoid cell disorder; osteoporogis; parkinson's disease; Alzheimer's disease; bone degenerative disorder; Human; genetic disorder; gene mapping; medical imaging; neurodegenerative disorder; lymphoid cell disorder; oste dermatitis. osteoporosis;

Homo sapiens.

WO200274961-A1.

26-SEP-2002.

14-MAR-2002; 2002WO-US005109

15-MAR-2001; 2001US-00810173

(HYSE-) HYSEQ INC.

Tang YT, Xue AJ, Wehrman T, Zhou P, G Yang Y, Ma T, Wang J, Ma Goodrich R, Asundi V, Ma Y, Yamazaki V, Che, , Wang D, Drmanac RT; i v, Zhang J; Zh Chen R, Wang Z, Zhao QA, Ghosh M;

New isolated polypeptides and polynucleotides, useful for preventin treating or ameliorating medical conditions, such as cancer, neurodegenerative disorders, lymphoid cell disorders, bone degenera disorders, and infections. WPI; 2003-040556/03. N-PSDB; ABX05088.

Claim 9; SEQ ID NO 629; 235pp; English.

The invention relates to human polynucleotides and the polypeptides encode. The polynucleotides and polypeptides are useful in diagnost forensics, gene mapping, medical imaging, identification of mutatic responsible for genetic disorders or other traits, assessing biodiv and producing many other types of data and products dependent on DN

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 The fusion was constructed using site-directed mutagenesis to fuse PAP-I encoding amino acid 1-136 with a protein C DNA sequence at the codon for amino acid 46. A plasmid contg. this construct was transfected into BHK cells which were then cultured to produce PAP-I protein C fusions which
                                                                                         Recombinant prodn. of hybrid phospholipid-binding proteins lipocortin phospholipid-binding domain and vitamin=K-depend
                                                                          Claim 21;
                                                                                                                                                    WPI; 1991-222905/30
                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                               29-DEC-1989;
                                                                                                                                                                                                     (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                        29-DEC-1989;
                                                                                                                                                                                                                                                                                                           WO9109953-A
                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid sequences. They are also useful for preventing, treating or ameliorating medical conditions, such as cancer, neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cellifications, osteoporosis, osteoparthritis, bone degenerative disorders, periodontal disease, liver fibrosis, infections (e.g. viral, fungal or bacterial) or autoimmune diseases (e.g. diabetes, atopic demnatitis). Sequences ABG9988-ABG9989 and ABU00010-ABU00433 represent human polypeptides of the invention. Note: The sequence data for this patent not represented in the printed specification but is based on sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gla-domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phopholipid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAP-I-protein C fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
30-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR13592 standard; protein; 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 117 AA;
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                                                                                                                                        AAQ12681.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 48
                                                                     Page 41; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE
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(first entry)
                                                                                                                                                                                                                            89US-00459082
                                                                                                                                                                                                                                                      89US-00459082
                                                                                                                                                                                                                                                                                                                                                                                   /note=
137. .1
                                                                                                                                                                                                                                                                                                                                     /label= protein C
/note= "amino acids 46-49"
141. 146
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                                                                                                                                                           /label= PAP-I
                                                                                                                                                                                                                                                                                                                                                                                   .140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; lipocortin; domain; vitamin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                           "amino acids 1-136"
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Pred. No. 1.6e-24;
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                                                                                           and vitamin=K-dependent
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                                                                                                    comprising
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the polynucleotide

protein

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RESULT 3
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                                                                                                                                               Polynuclectide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynuclectide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; and immunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein activity.
neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 ar used in the course of the invention for the identification and
                                                                                    identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat disorders such as
                                                                                                      or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous other diagnost
                                                                                                                                                                                                                                                                                                 Claim 11; Page 1248-1249; 1425pp; English
                                                                                                                                                                                                                                                                                                                                                 antigens, useful for treatment, prevention,
                                                                                                                                                                                                                                                                                                                                       such as lung cancer.
                                                                                                                                                                                                                                                                                                                                               Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-587514/55.
N-PSDB; AAF18269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2000; 2000WO-US005918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; lung cancer associated protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB58393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB58393 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anticoagulant assays. This sequence contains and additional fragment of amino acids Lys or Arg, between the light and heavy chains. At least three amino acids are present. See also AAQ12678-81. (Updated on 25-MAR. 2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 146 AA;
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ROSEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   associated polypeptide sequence SEQ ID
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llarity 100.0%;
Conservative 0
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Pred. No. 2.1e-24
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RESULT 4
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04-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence given is the amino acid sequence of CPB-I. CPB-I was used within a method which involved adding basic amino acids to it which resulted in its stabilisation. This lead to the production of CPB-I which keeps its activity when it is frozen, molten or has been processed by several procedures. (Updated on 10-MAR-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stabilisation of CPB-I for drug compsn. - selected from lysine, arginine and/or orni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUL-1992.
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                                                            10-MAR-2003
04-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 319
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                  CPB-1.
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) KAGAKU OYOBI
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Pred. No. 3.2e-24;
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Pred. No. 5.3e-24;
, Mismatches 0;
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    n. - by adding basic aminoacid ornithine.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPB-1; saccharides; stabilisation; antihemagglutination; corneal disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucosamine, xylose, saccharose,or dextran. The processed by sever of CPB-I which kept its activity when it had been processed by sever treatments. CPB-I can be used as a medicine for antihemagglutination treatments. CPB-I can be used as a medicine for antihemagglutination are made and corneal diseases. (Updated on 10-MAR-200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence given is the amino acid sequence of CPB-1. CPB-1 was us within the method of the invention which involved adding saccharides it which resulted in its stabilisation. The saccharide was pref. glucosamine, xylose, saccharose, or dextran. This lead to the product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 2; 4pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stabilisation of CPB-1 for drug compsn. - cont from glucose, glucosamine, xylose, saccharose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-288938/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dermal and corneal diseases.
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(KAGA ) KAGAKU OYOBI KESSEI RYOHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      field.)
                                                                                                                                                                                                                                                                                                                    AAR41021 standard; protein; 319
                                                                                                                                                                                                                          Calphobindin I;
                                                                                                                                                                                                                                                 Calphobindin I (CPB-I)
                                                                                                                                                                                                                                                                         29-MAR-1994
                                                                                                                                                                                                                                                                                                AAR41021;
                                                                                                                                                                            JP05213769-A
                                                                                                                                                                                                   Homo sapiens
          Protein kinase C inhibitor effective against malignant (opt. recombinant) calphobindin I.
                                                                                                                                                    24-AUG-1993.
                                                                                                       04-FEB-1992;
                                                                                                                              04-FEB-1992;
                                              WPI; 1993-299558/38
                                                                      (KAGA-)
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                                                                     KOWA CO LTD.
ZH KAGAKU OYOBI
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                                                                                                         92JP-00019032.
                                                                                                                               92JP-00019032
                                                                                                                                                                                                                            CPB-I; Protein kinase
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                                                                        KESSEN RYOHO KENKYUSHO
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Pred. No. 5.3e-24;
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                                                                                                                                                                                                                                PKC; inhibition; tumour.
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a x o o o o o o o o

Claim 1;

Page 2-3; 6pp; Japanese.

Sequence

319 AA;

intramuscularly, percutaneously or rectally

Calphobindin I (CPB-I) or recombinant calphobindin I (r-CPB-X) inhibits protein kinase C (PKC) and is useful in the treatment of malignant tumours caused by abnormal activation of PKC. CPB-I is extracted from human or animal organs and may be applied intravenously, orally,

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A X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X 
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ABG32550
                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                           The invention relates to eye drops contain CPB-I (anexin V) and a polyhydric alcohol having a carbonyl value of not more than 5micro Mol/g. The eyes drops are for treating e.g. corneal diseases. Such eye drops are without unpleasant irritation upon dropping but with satisfactory long-term storage stability. The present sequence is the human CPB-I (calcium/phospholipid binding) protein
                                                                                                                                                                                                                                                             Sequence 319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 13-14; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eye drops for treating e.g. corneal diseases, contain CPB-I and polyhydric alcohol with specific carbonyl value, without unpleasant irritation upon dropping but with satisfactory long-term storability.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; CPB-I; eye drop; ophthalmological; anexin V; corneal disease; calcium/phospholipid binding protein; polyhydric alcohol.
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24 RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE
                              1 RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 48
                                                                                                                                         48;
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CHEMO-SERO-THERAPEUTIC RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sano M, Shinoda Y,
                                                                                                                                   Conservative
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                                                                                                                       100.0%; Score 231; DB 5;
100.0%; Pred. No. 5.3e-24;
tive 0; Mismatches 0;
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Pred. No. 5.3e-24;
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Query Match Best Local S Matches 48

Local Similarity

100.0%;

Conservative

0;

Score 231; DB 7; Pred. No. 5.3e-24;); Mismatches 0;

Length 319;

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0

Sequence 319 AA;

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C Claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence C which is differentially regulated in an animal subjected to pain and a C that increases or decreases the expression of the polymucleotide sequence C that is differentially expressed in neuronal tissue of a first animal C the expression of a polymucleotide sequence which is differentially expressed in neuronal tissue of a first animal C the expression of a polymucleotide sequence which is differentially C expressed in an animal subjected to pain, a method for identifying a compound which regulates C compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical compound or small molecule that regulates the c polymucleotide given in the C specification, a method for identifying a compound useful in treating C polypeptides or their antibodies. The polymucleotide or the compound that c polypeptides given in the C pain and a pharmaceutical composition comprising the one or more C pain (e.g. spinal segmental nerve injury (CNID) and spared nerve injury (SNI)) in an animal (e.g. gene C polymic activity is useful for preparing a medicament for treating C pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene C the specification, but was obtained in electronic form directly from WIPO at ftp. wino.inf/muh/muhlished nct semmences.
                         ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENBANK; P08758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pain; neuronal tissue; gene therapy;
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RESULT 9
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ID ADE5
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                                                     that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal composition of a polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal composition of a polymucleotide sequence which is differentially the expressed in a polymucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the composition, a method for identifying a compound or small molecule that regulates the activity in an animal subjected to pain, a method for identifying a compound understance of the compound for identifying a compound unseful in treating specification, a method for identifying a compound useful in treating composition, a method for identifying a compound useful in treating composition comprising the one or more of polypeptides or their antibodies. The polypucleotide or the compound that polypeptides or their antibodies. The polymucleotide or the compound that polypeptides or their antibodies. The polymucleotide or the compound that polypeptides or their antibodies. The polymucleotide or the compound that polypeptides or their antibodies. The polymucleotide or the compound that polypeptides or their antibodies. The polymucleotide or the compound that polypeptides or their antibodies. The polymucleotide or the compound that polypeptides or their antibodies. The polymucleotide or the compound that polypeptides or their antibodies of the polymucleotide or the compound that polypeptides or the compound that polypeptides or their activity is useful for preparing a mediciament for treating compound that polypeptides or the compound that polypeptides or the
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising preparing a medicament for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENBANK; P08758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or human polynucleotides or a polynucleotide which represents a derivative or allelic variation of the nucleic acid sequence. Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention discloses a composition comprising two or more isolated rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which is differentially regulated in an animal subjected to pain and a
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segmental nerve injury; chronic constriction injury; CCI;
nerve injury; SNI; Chung.
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Sequence 319

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Best Local Similarity
RESULT 11
AAP80511
ID AAP8
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                                                                                                                    Matches
                                                                                                                             Query Match
Best Local 9
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13-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP82317 standard; protein; 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAP-I isolated from biological fluid, used as anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP82317;
                                                                                                                                                                                                       The protein does not contain a leader peptide sequence, indicating paper is probably not constitutively secreted. The Met residue is real in a post-translational event and the newly formed NH2-terminal at in a blocked by acetylation. It binds to phospholipid and inhy phopholipase A2. The protein can substitute heparin or other anticoagulants in the treatment of disseminated intravascular coagulation, deep vein thrombosis, or other disorders. It also has antinflammatory properties. (Updated on 25-MAR-2003 to correct PA antinflammatory properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-FEB-1987;
05-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pAp-I; anticoagulant; anti-inflammatory agent; phospholipid;
phospholipase A2; disseminated intravacular coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO8805659-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    deep vein thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAN82107
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1988-235049/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Fujikawa K,
                                                                                                                                                                                                                                                                                                                                                        Human proteins having anticoagulant and antiinflammatory activity isolated from biological fluids by anion-exchange chromatographic
                                                                                                                                                                    Sequence 320
                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNIW ) UNIV WASHINGTON
AAP80511 standard; protein; 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                 field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 RKAMKGLGTDEESILTLLTSRSNAOROEISAAFKTLFGRDLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
                                                                   25
                                                                               1 RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKAMKGLGTDEESILTLLTSRSNAQROEISAAFKTLFGRDLLDDLKSE 48
                                                                                                                                  Similarity
                                                                 RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                 Page ?; 62pp; English.
                                                                                                                    100.0%; ilarity 100.0%; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Irani MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87US-00011782
87US-00059355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88WO-US000340
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Pred.
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                                                                                                                         Score 231; DB l;
Pred. No. 5.3e-24;
; Mismatches 0;
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     B
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No. 5:3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
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                                                                                                                                                Length 320;
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                                                                                                                            Indels
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AAP80511;

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RESULT 12
AAP80242
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Best Local Similarity
                                                                                                                                                                                                                                                                    Matches
           WO8807576-A.
                                Homo sapiens
                                                      Vascular anticoagulating protein (VAP) VAC-alpha; anticoagulant activity;
                                                                             Sequence vascular anticoagulating protein (VAP) VAC-alpha (Asp?2).
                                                                                                                                                                                                                                                                                                                      This polypeptide exhibits strong anticoagulant activities and is useful for the treatment and prevention of e.g. thrombosis or disseminated intravascular coagulation in the brain, heart and peripheral blood vessels, such as cerebral and myocardial infarction. It has no antigenicity against man and can be produced in large amts. using recombinant methods. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                    antiinflammatory;
                                                                                                           25-MAR-2003
12-SEP-1990
                                                                                                                                                             AAP80242 standard; protein;
                                                                                                                                              AAP80242;
                                                                                                                                                                                                                                                                                                           Sequence 320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page ?; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant placental coagulation inhibitor - useful for the prevention and treatment of thromboses or disseminated intravascular coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1988-236733/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-FEB-1987;
23-JUL-1987;
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10-MAR-2003
12-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Placental coagulation inhibitor; disseminated vascular coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Placental coagulation inhibitor.
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                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                              Iwasaki A,
                                                                                                                                                                                                                                                           100.0%; Score 231; DB 1; ilarity 100.0%; Pred. No. 5.3e-24; Conservative 0; Mismatches 0;
                                                                                                         (revised)
(first entry)
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(revised)
(first entry)
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87JP-00184428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88EP-00102468
                                                  phospholipase inhibitory
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                                                                                                                                                                                                                                                                                Length 320;
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RESULT 13
AAP90053
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Best Local Similarity
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25-MAR-2003
01-NOV-1989
                               03-NOV-1987;
                                                     29-OCT-1988;
                                                                            07-JUN-1989
                                                                                                    EP318703-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            The DNA is produced by determining the amino acid sequence of isolated and highly purified VAPs, constructing DNA probes on the basis of this sequence, using the probes to search through suitable cDNA libraries, isolating cDNA that hybridises with the probes, by inserting the cDNA into a suitable vector, and using the vector to transform a host organism. VAC-alpha has anticoagulant activity under certain conditions, but loses this activity in the event of severe bleeding. It acts by the conditions of the conversion of factor X to factor X and conversion of prothrombin to thrombin. It is structurally related to lipocortin I (Nature, 320, 77, 1986) and lipocortin II (cell, 46, 191/120, 1986) and has similar antiinflammatory and phospholipase inhibitory activity.

(Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
        (BEHW ) BEHRINGWERKE AG
                                                                                                                                                Anticoagulant;
                                                                                                                          Homo sapiens;
                                                                                                                                                                     anticoagulant
                                                                                                                                                                                                                                                               AAP90053 standard; protein; 320
                                                                                                                                                                                                                                             AAP90053;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 320 AA;
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28-MAR-1987;
04-NOV-1987;
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Falkner E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 41; Page 171-72; 183pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New vascular anti:coagulating proteins - antiinflammatory agents, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1988-292861/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-1988;
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(revised)
(first entry)
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                                                                                                                          (human)
                                                                                                                                                                     PP4 protein
                             87DE-03737239
                                                                                                                                                 PP4
                                                   88EP-00118039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maurerfogy I, Bodo G,
dole G, Reutlingsp CMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87DE-03710309.
87DE-03710364.
87DE-03710430.
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                                                                                                                                              protein; thromboplastin
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                                                                                                                                                                                                                                                                                                                                                                   Score 231; DB 1;
Pred. No. 5.3e-24;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful as
                                                                                                                                                                                                                                                                                                                                                                                        Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stratowa
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Best Local S
Matches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of anticoagulant PP4 protein. This inhibits to coagulation at the thromboplastin stage. (Updated on 25-MAR-2003 correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) on 25-MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 11 and Table 1; 12pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA sequence encoding anticoagulant PP4 protein - protein, vectors, antibodies, etc., useful therapeuti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1989-166767/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grundmann
                                                                                                                                                                                                                                                                                                                                                                                             Human lipocortin-V; lambdaHLipo V-l; anti-inflammatory agent.
                                                                                                                                                                                                                                                                                                                      30-AUG-1989.
                                                                                                                                                                                                                                                                                                                                                EP330396-A.
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                         Human lipocortin-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP91363 standard; protein; 320
                       Human lipocortin-V was isolated from a lambda gt10 human peripheral blood lymphocyte cDNA library with rat lipocortin-V cDNA of lambda RLipo V-l as probe. Lipocortins are anti-inflammatory agents and can be used to treat arthritic, allergic, dermatologic, ophthalmic, and collagen diseases. See also AAN90598, AAN90599, and AAP91362
                                                                                                                         Human lipocortin cpds. III, IV, V, arthritic, allergic, dermatologic, involving inflammatory processes.
                                                                                                                                                                                                                                                                      26-FEB-1988;
                                                                                                                                                                                                        Wallner BP, Pepinsky RB,
                                                                                                                                                                                                                                (BIOJ )
                                                                                                                                                                                                                                                                                               20-FEB-1989;
                                                                                                 Claim 16; Fig 4; 32pp; English.
Sequence 320
                                                                                                                                                                             WPI; 1989-250486/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 100.0%; Score 231; DB 1; Local Similarity 100.0%; Pred. No. 5.3e-24; 1es 48; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                BIOGEN INC.
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   A,
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                                                                                                                                           and VI - used in treatment of ophthalmic and collagen disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapeutically
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Query Match Best Local Similarity Matches 48; Conserv

Conservative

100.0%; Score 231; DB 1; 100.0%; Pred. No. 5.3e-24; tive 0; Mismatches 0;

Length Indels

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Gaps

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Search completed: April Job time : 56 secs

8, 2004, 11:56:50

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AAP91953
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Best Local Similarity
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25-MAR-2003
10-MAR-2003
30-JUL-1989
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                                                                                                                                        This vascular anti-coagulating protein (VAC)-alpha is used in the preparation of monoclonal antibodies (MAbs). The VAC-alpha is inject into a host animal, in conjugation with ey keyhole limpet haemocyan and the B-cells from immunised hosts are then fused with myeloma ce The resultant hybridomas (VAA-8 and VAA-9) produce Abs specific to alpha. Abs can be used as immunoassay reagents to detect VAC protein affinity ligands for protein purificm. and as medicaments for bindi and/or neutralising VAC proteins in vivo. See also ANN91354 and Epandors neutralising VAC proteins in vivo. See also ANN91354 and Epandors neutralising VAC proteins in vivo. See also ANN91354 and Epandors neutralising VAC proteins in vivo. See also ANN91354 and Epandors neutralising VAC proteins in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vascular anti-coagulating proteins; hybridomas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vascular anti-coagulating protein-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP91953;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus.
                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAN91353.
                                                                                                                                                                                                                                                                                                                                                                             WPI; 1989-293724/41.
                                                                                                                                                                                                                                                                                                                                                                                                       Gunther A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DE3810331-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                      Sequence 320 AA;
                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 11pp; German.
                                                                                                                                                                                                                                                                                                                      Monoclonal antibodies to vascular anti-coagulating hybridomas producing such antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                 (BOEH ) BOEHRINGER INGELHEIM
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                                                    48;
               1 RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE
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                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                100.0%; Score 231; DB 1; 100.0%; Pred. No. 5.3e-24;
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OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                             150
149.5
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231
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004 Compugen Ltd
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annexin VII - mous
annexin IV - human
annexin VI (valida
calcimedin, 32K -
annexin - chicken
                                                                            annexin XI - human
annexin XII - Hydr
annexin VIII - hum
annexin VII - Afri
annexin IX - fruit
hypothetical prote
annexin X - fruit
annexin III - huma
annexin VII - slim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           annexin VI - mouse
annexin VII, long
annexin VI - rat
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annexin V - bovine
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                                               Biochemistry 26, 8087-8092, 1987

A,Title: Primary structure of human placental anticoagulant protein.

A;Reference number: A29417; MUID:88163463; PMID:2964863

A;Contents: amino-terminal acetylation

A;Accession: A29417

A;Molecule type: mRNA

A;Residues: 1-320 <FUNS

A
                     A; Title: Structure and expression of cDNA for an inhibitor of blood coas
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43.3				45.0			47.6		48.1	48.1	48.1	48.5	48.5	49.8	49.8	49.8	
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ALIGNMENTS

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RESULT 1	
annexin V [validated] - human	anticoaculant pr
N; Alternate names: endonexin II; lipocortin v; piacemtai americas	all
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text	Change 08-Dec-20
C; Accession: D29250; A30206; A28076; S01016; A2941/; A415	L.K.; Miller, G
R;Pepinsky, R.B.; Tizaro, k.; Mactaliano, k.o., Simone, Francisco ho	· · · · · · · · · · · · · · · · · · ·
A; Title: Five distinct calcium and phospholipid binding p	DIOLETINE PHOTE IN
A; Recession: D29250	
A; Molecule type: mRNA	
A;Residues: 1-320 < KBF > A;Residues: 1-320	5.1; PID:g307116
R;Grundmann, U.; Abel, K.J.; Bohn, H.; Loebermann, A.; Loebermann, C.; R;Grundmann, G.; R;Grundmann, G.; Loebermann, G.; Loebe	occoperent,
A; Title: Characterization of cDNA encoding human placents	human placental anticoagulant
A;Reference number: A30206; MULD:88234493; FMLD:2307473	
A; Molecule type: mRNA	
A, Residues: 1-320 <gru></gru>	5.1; PID:g189615
A;Cross-references: GB:ML5334; MLD.310751; Fig. D.D.; Haigler, H.T. R:Kaplan, R.; Jaye, M.; Burgess, W.H.; Schlaepfer, D.D.; Haigler, H.T.	Haigler, H.T.
J. Biol. Chem. 263, 8037-8043, 1988	xin II, a Ca(2+)
A; TITTE: CIOILING and CAPACITY TO PMID: 2967291 A; Reference number: A28076; MUID: 88228020; PMID: 2967291	*
A; Accession: A28076	
A; Molecule type: mxnA	
A;Cross-references: GB:J03745; NID:g182111; PIDN:AAA52386.1; PID:g182112	6.1; PID:GISZIIZ
R; Maurer-Fogy, I.; Reutelingsperger, C.P.M.; Fielers, O., Ecc., C.,	, 5000, 0., 0.,
Eur. J. Biochem. 174, 585-592, 1900	ar anticoagulant
A; Itte: Cruing C.F. 01016; MUID:88271329; PMID:2455636	
A; Accession: S01016	
A; Molecule type: mRNA	
A; Residues: 1-320 (MA) A; Res	85.1; PID:g37637
A; Note: part of this sequence was confirmed by protein sequencing	kawa. K.
R;Funakoshi, T.; Hendrickson, L.E.; McMarress, E.S.,	

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F;101-117/Region: endonexin fold #status predicted F;173-245/Domain: annexin repeat homology <AX3> F;185-201/Region: endonexin fold #status predicted F;249-320/Domain: annexin repeat homology <AX4> F;260-276/Region: endonexin fold #status predicted F;2/Modified site: acetylated amino end (Ala) (in m F;23/Binding site: phosphate (Thr) (covalent) #status F;28,30,32,72/Binding site: calcium, high affinity
                                                                                                                                                                                                                                                                                                                                                                                                                             \;\text{Map position: 4q26-4q28} \;\text{Introns: 3/3; 32/1; 63/3; 101/3; 132/1; 158/3; 177/3; 209/1; 241/1; 260/3; 301/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                derstood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: The gene encoding human annexin V has a TATA-less A;Reference number: I37172; MUID:95047484; PMID:7958998 A;Accession: I37172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 29-73;274-297;300-320_<FU2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Contents: annotation; X-ray crystallography, 2.0 angstroms
A;Note: three calcium ions are strongly bound at sites in the first, second,
R;Funakoshi, T.; Heimark, R.L.; Hendrickson, L.E.; McMullen, B.A.; Fujikawa,
Biochemistry 26, 5572-5578, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
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                                                                                                                                                                                                                                                            ;18-89/Domain: annexin repeat homology <AXI>;29-45/Region: endonexin fold #status predicted;90-161/Domain: annexin repeat homology <AX2>
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A;Residues: 86-131,'W',260-272,274-297,300-315,'X',317-320 <SCH>
R;Ahn, N.G.; Teller, D.C.; Bienkowski, M.J.; McMullen, B.A.; Lipkin,
J. Biol. Chem. 263, 18657-18663, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Schlaepfer, D.D.; Mehlman, T.; Burgess, W.H.; Proc. Natl. Acad. Sci. U.S.A. 84, 6078-6082, 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:D00172; NID:g219480; PIDN:BAA00122.1; PID:g/219481
A;Note: part of this sequence was confirmed by protein sequencing
R;Schlaepfer, D.D.; Mehlman, T.; Burgess, W.H.; Haigler, H.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene: GDB:ANX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GDB:120555; OMIM:131230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ipid-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: EMBL:U01691; NID:g430964; PIDN:AAB40047.1; PID:g430966
Comment: Annexins undergo reversible, calcium-dependent binding to membr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Residues: 1-320 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title: Human placental anticoagulant protein: isolation and Reference number: A29670; MUID:88050845; PMID:2960376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title: The calcium binding sites in human annexin V by crystal structure analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huber, R.; Schneider, M.; Mayr, I.; Roemisch, J.; 388 Lett. 275, 15-21, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Molecule type: protein;Residues: 7-25;27-42;5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Rothhut, B.; Comera, C.; Cortial, S.; Haumont, P.Y.; Diep Le, K.H.; Cavadore, J. 263, 929-935, 1989; Jitle: A 32 KDa lipocortin from human mononuclear cells appears to be identically Reference number: S06646; MUID:90088443; PMID:2532007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: proteir
Residues: 85-93 <AHN>
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Accession: C31953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: A28038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OC. Natl. Acad. Sci. U.S.A. 84, 6078-6082, 1987 Title: Structural and functional characterization of endonexin II,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: A41514
                                                                                                                                                                                                                                                                                                                                                                                     perfamily: annexin I; annexin repeat homology words: acetylated amino end; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                      Product: annexin V #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253-260, 1994
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Schneider, M.; Mayr, I.; Roemisch, J.; Paques, E.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rather
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V has been proposed to play a role in the inhibition of blood coagul, her than proteolytic inactivation. It does not affect thrombin-dependent
                                           d amino end (Ala) (in mature form) #status (Thr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                     calcium
               (Met, Gly,
                                                                                                                                                                                                                                                                                                                                                                     oinding; duplication; endonexing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter with a high G+C
               Gly, Glu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       characterization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane phospholip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be identical with
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                                                                      experimental
            #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  calcium-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , and fourth K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
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                  C;Species: Gallus gallus (Chicken)

C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 02-Jun-2000

C;Accession: A35381; A28623; B40404; S32523; S08771

R;Fernandez, M.P.; Selmin, O; Martin, G.R.; Yamada, Y.; Pfaeffle, M.; Deut. J. Biol. Chem. 265, 8344, 1990
A; Reference number:
                                                                                                                                                                N;Alternate names: anchorin CII; endonexin II; lipocortin
                                                                                                                                                                                                              annexin V - chicken
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F;248-319/Domain: annexin repeat homology AX4>
F;259-275/Region: endonexin fold #status predicted
F;1/Modified site: acetylated amino end (Ala) #status experimental
F;22/Binding site: phosphate (Thr) (covalent) #status experimental
F;27,29,31,71/Binding site: calcium, high affinity (Met. Gly, Gly) #status predicted
F;32,34,35/Binding site: calcium, low affinity (Thr, Glu, Glu) #status predicted
F;99,101,103,143/Binding site: calcium, high affinity (Leu, Glu) #status predicted
F;99,101,103,143/Binding site: calcium, high affinity (Leu, Gly, Gsp) #status
                                                                                                                                                                                                                                                                                                                                                                                                   F;184-200/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Comment: Annexin V has been proposed to play a role olipid-binding rather than proteolytic inactivation. C;Superfamily: annexin I; annexin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 1-35,'T',37-124,'E',126-320 <LE2>
A;Note: It is uncertain whether the sequence (C;Comment: Annexins undergo reversible, calcin
                                                                                                                                                                                                                                                                                                                                                                                                                        F;172-244/Domain: annexin repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                F:89-160/Domain: annexin repeat homology <AX2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;17-88/Domain: annexin repeat homology <AXi>F;28-44/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           derstood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: S27214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochim. Biophy A; Title: Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Jun-1994 #sequence_revision 10-Feb-1995 #text_change 26-Feb-1999
C;Accession: S27214; S27215
R;Learmonth, M.P.; Howell, S.A.; Harris, A.C.M.; Amess, B.; Patel, Y.; Giam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
S27214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S27215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S27214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate
C;Species: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;33,35,36/Binding site: calcium, low affinity (Thr, Glu, Glu) #status expe
F;73,78/Binding site: calcium, low affinity (Leu, Glu) #status experimental
F;100,102,104,144/Binding site: calcium, high affinity (Leu, Gly, Gly, Asp)
F;259,261,263,303/Binding site: calcium, high affinity (Met, Gly, Gly, Asp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           annexin V -
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                                                                                                       Matches
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                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keywords: acetylated amino end; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                             260,262,302/Binding site: calcium, high affinity (Met, Gly,
                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biophys. Acta 1160, 76-83, 1992
Novel isoforms of CaBP 33/37 (Annexin V) from mammalian
                                                                                                    46;
                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             names: CaBP33; CaBP37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
RKAMKGLGTDEESILTLLTSRSNAORQEIAVAFKTLFGRDLLDDLKSE
                         RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     endonexin fold
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                                                                                                                       95.8%;
                                                                                                                                            97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S.A.; Harris, A.C.M.; Amess, B.; Patel, Y.; Giambanco, 0, 76-83, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the sequence differences are due to allelic variation reversible, calcium-dependent binding to membrane phosphol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUID:93041974; PMID:1420335
                                                                                                                                                                                                                                                                                                                                                                                         homology <AX3>
#status predicted
                                                                                                                Score 224; DB 1;
Pred. No. 2.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 231; DB 1;
Pred. No. 3.2e-21;
                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             calcium binding; duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            role
                                                                                                                                   Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in the It does
                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glu) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibition of blood coagulat not affect thrombin-depender
  71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48
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                                                                                                                                                                               Gly,
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                                                                                                                                                                               Asp)
                                                                                                                                                                                                                                                                    #status predicted
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phospholipi
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A35381; MUID:90243721; PMID:2159478

V; placental anticoagulant

prot

Deutzmann,

Thu

Apr

A;Cross-references: GB:M30971; GB:J03194; NID:G211138; PIDN:AAA48591.1; PID:G211139 R;Fernandez, M.P.; Selmin, O.; Martin, G.R.; Yamada, Y.; Pfaeffle, M.; Deutzmann, R

A; Accession: A35381

A;Molecule type: mkwA

Residues: 1-321 <FER>

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A;Residues: 1-118,'LLKCRILNRFNMOEYBANLGRNKITGRRHQAIFRDCWWSCCRQIEI',163-167,'E',169-321
A;Cross-references: GB:M30971; GB:J03194; NID:g211138
R;Genge, B.R.; Wu, L.N.Y.; Adkisson IV, H.D.; Wuthier, R.E.
J. Biol. Chem. 266, 10678-10685, 1991
J. Biol. Chem. 266, 10678-10685, 1991
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A,Title: The structure of anchorin CII, a collagen binding protein isolated from chondre A; Reference number: A28623; MUID:88186917; PMID:2833522
A; Accession: A28623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: epiphyseal growth plate cartilage (matrix vesicle-enriched micros R;Boustead, C.M.; Brown, R.; Walker, J.H.
Biochem. J. 291, 601-608, 1993
A;Title: Isolation, characterization and localization of annexin V from chicken liver.
A;Reference number: S32523; MUID:93249384; PMID:8484740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Matrix vesicle annexins exhibit proteolipid-like properties. Selective partitic A;Reference number: A40404; MUID:91244852; PMID:2037607 A;Accession: B40404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
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A;Residues: 188-199 <GEN>
                                                                                                                                                                                        N,Alternate names: endonexin II; lipocortin V; placental anticoagulant protein; placent C;Species: Rattus norvegicus (Norway rat) C;Pate: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999 C;Pate: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999 C;Accession: C29250; S66680 R;Pepinsky, R.B.; Tizard, R.; Mattaliano, R.J.; Sinclair, L.K.; Miller, G.T.; Browning, R;Pepinsky, R.B.; Tizard, R.; Mattaliano, R.J.; Sinclair, L.K.; Miller, G.T.; Browning, J. Biol. Chem. 263, 10799-10811, 1988 J. Biol. Chem. 263, 10799-10811, 1988 J.;Title: Five distinct calcium and phospholipid binding proteins share homology with li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ś
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;Molecule type: protein
;Residues: 6-20;85,'X',87-88,'X',90-93,'X',95-96,'XX',99-100,'X',102-103,'XX',106-107;
;Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comment: Annexin V has been proposed to play a role in the inhibition of blood coagulation. It does not affect thrombin-dependers the content of the content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;260-276/Region: endomexin fold #status predicted
;260-276/Region: endomexin fold #status predicted
;28,30,32,72/Binding site: calcium, high affinity (Met, Glu, Glu) #status predicted
;33,35,36/Binding site: calcium, low affinity (Thr, Glu, Glu) #status predicted
;73,78/Binding site: calcium, low affinity (Leu, Glu) #status predicted
;100,102,104,144/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status predicted
;259,261,263,303/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: $32523
                                                                                                  A;Accession: C29250
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101-117/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2-321/product: annexin V #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keywords: calcium binding; collagen binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local !
                                                                                                                                    Fitle: Five distinct calcium and phospholipid binding; Reference number: A92659; MUID:88273202; PMID:2968983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .8-89/Domain: annexin repeat homology <AX1>
29-45/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40;
1-319 <PEP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 206; DB 1; Length 321; Pred. No. 4.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        duplication; endonexin fold; membrane-as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                proteins share homology with li
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Eur. J. Biochem. 232, 327-334, 1995
A;Title: Structure of rat annexin V gene and molecular diversity of its
A;Reference number: S66680; MUID:96035863; PMID:7556178
A;Accession: S66680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M21730; NID:g205138; PIDN:AAA41512
R;Imai, Y.; Kohsaka, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;26,28,30,70/Binding site: calcium, high affinity (Met, Gly, Gly, Glu) # F;31,33,34/Binding site: calcium, low affinity (Thr, Glu, Asp) #status pr F;71,76/Binding site: calcium, low affinity (Leu, Glu) #status predicted F;71,76/Binding site: calcium, high affinity (Leu, Gly, Gly, Asp F;257,259,261,301/Binding site: calcium, high affinity (Met, Gly, Gly, Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F:171-243/Domain: annexin repeat homology <AX3>
F:183-199/Region: endonexin fold #status predicted
F:247-318/Domain: annexin repeat homology <AX4>
F:258-274/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 1/3; 30/1; 61/3; 99/3; 130/1; 156/3; 175/3; 207/1; 239/1; 258/
C;Superfamily: annexin I; annexin repeat homology
C;Keywords: calcium binding; duplication; endonexin fold; membrane-associ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   olipid-binding rather than proteolytic inactivation. It does
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C;Comment: Annexins undergo reversible, calcium-dependent binding to memb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-319 <IMA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text change 22-Jun-1
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text change 22-Jun-1
C;Accession: A31578; D45066; $59624; A45066; B45066; C45066; C450666; C45066; C45066; C45066; C45066; C45066; C45066; C45066; C45066; C45066; C45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;88-159/Domain: annexin repeat homology <AX2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Carbohydrate-binding proteins in bovine kidney have consensus A;Reference number: A45066; MUID:93015942; PMID:1400371 A;Accession: D45066
R;Sohma, H.; Matsushima, N.; Watanabe, T.; Hattori, A.; Kuroki, Y.; Akin Biochem. J. 312, 175-181, 1995
A;Title: Ca(2+)-dependent binding of annexin IV to surfactant protein A A;Reference number: S59624; MUID:96077142; PMID:7492310
                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 10-18,'X',20-22,'X',24-25;29-48;101-107,'X',109-118;'X',194-
A;Experimental source: kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kojima, K.; Ogawa, H.K.; Seno, N.; Yamamoto, K.; Irimura, J. Biol. Chem. 267, 20536-20539, 1992
                                                                                                                                                                               A;Note: these fragments are derived from a A;Note: 12-Met and 12-Tyr were also found
                                                                                                                                                                                                                                                                     A, Note: sequence extracted from NCBI backbone (NCBIP:116211, NCBIP:11620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:X13627; NID:g215; PIDN:CAA31954.1; PID:g216; GB:MR;Kojima, K.; Ogawa, H.K.; Seno, N.; Yamamoto, K.; Irimura, T.; Osawa, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-319 <HAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
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Comment: Annexin V has been proposed to play a role in the inhibition o
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Best Local S
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79.2%;
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                                                                                                                                                                                                                                             from a 33K protein
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RESULT 7
S29170
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F;183-199/Region: endonexin fold #status predicted
F;247-318/Domain: annexin repeat homology <AX45
F;258-274/Region: endonexin fold #status predicted
F;258-274/Region: endonexin fold #status predicted
F;1/Modified site: blocked amino end (Ala) (probably acetylated) #sgatus experimental
F;6/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;124,244/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                               문
   C;Species: Mus musculus
                                                                        annexin VII - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Weber, K.; Johnsson, N.; Plessmann, U.; Van, P.N.; Soling, H.D.; Ampe, C.; EMBO J. 6, 1599-1604, 1987
A; Title: The amino acid sequence of protein II and its phosphorylation site for the first phosphorylation site for the f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: 32K calelectrin; chromobindin IV; endonexin; lipocortin IV; protein C;Species: Sus scrofa domestica (domestic pig) C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 24:Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derstood
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A; Residues: 1-318 <WEB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Weber,
                                    ;Alternate names: synexin
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A;Molecule type: protein
A;Residues: 29-44;72-77;112-119;163-180;181-190;226-235 <SOH>
C;Comment: Annexins undergo reversible, calcium-dependent binding
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Keywords: blocked amino end; calcium binding; duplication; endonexin fold; glycoprote; 16-87/Domain: annexin repeat homology <AX1, 27-43/Region: endonexin fold #status predicted
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199-115/Region: endonexin fold #status predicted
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;7/Binding site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248-319/Domain:
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                                                                                                                                                                                                                                                                                            RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 48
                                                                                                                                                                                                                                   RKAMKGLGTDEDAIISVLAYRSTAQRQEIRTAYKSTIGRDLLDDLKSE
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                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endonexin fold #status predicted annexin repeat homology <Ax3>
(house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                          74.5%;
70.8%;
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70.88;
                                                                                                                                                                                                                                                                                                                                                                               Score 172; DB 1;
Pred. No. 7.6e-14;
7; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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Pred. No. 5.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         calcium-dependent binding to membrane phospholip
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••
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 318;
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                                                                                                                                                                                                                                                                                                                                                                                   Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                        Gaps
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A;Molecule type: mRNĀ
A;Residues: 1-97,'Q',99-321 <GRU>
A;Cross-references: EMBL:M19383; NID:g189616; PIDN:AAC41689.1; PID:g189617
R;Ahn, N.G.; Teller, D.C.; Bienkowski, M.J.; McMullen, B.A.; Lipkin, E.W.;
                                                                                                                                             R;Grundmann, U.; Amann, E.; Abel, K.J.; Kuepper, H.A. Behring Inst. Mitt. 82, 59-67, 1988
A;Title: Isolation and expression of cDNA coding for a A;Reference number: S07434; MUID:88309022; PMID:2970257
A;Accession: S07434
                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 30-Jan-1993 #sequence revision 26-May-1994 #text_change 22-Jun-1999
C;Accession: A42077; B42077; S07434; A31953; A31046
R;Tait, J.F.; Smith, C.; Frankenberry, D.A.; Miao, C.H.; Adler, D.A.; Diste
                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 87-129 < TA2 >
                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M82809; NID:g178698; PIDN:AAA51740.1; PID:g178699
                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-321 <TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics 12, 313-318, 1992
A;Title: Chromosomal mapping of the human annexin IV (ANX4)
A;Reference number: A42077; MUID:92155721; PMID:1346776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: endonexin I; placental anticoagulant protein II; PP4-X protein
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F;163-224/Domain: annexin repeat homology <AX1>
F;235-306/Domain: annexin repeat homology <AX2>
F;318-390/Domain: annexin repeat homology <AX3>
F;318-390/Domain: annexin repeat homology <AX3>
F;394-463/Domain: annexin repeat homology <AX4>
                                                                                                                                                                                                                                                                                                                                     A; Accession: B42077
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A42077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       annexin IV -
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A,Residues: 1-144,'8',146-303,'A',305-463 <ZHW>
A,Cross references: EMBL:L13129; NID:g293293; PIDN:AAA37238.1; PID:g293294
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R;Zhang-Keck, Z.Y.; Burns,
submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem J. 289, 735-741, 1993
A;Title: Mouse synexin (annexin VII) polymorphisms and a A;Reference number: S29170; MUID:93168121; PMID:7916616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position:
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A;Accession: S51173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:L13129
R;Zhang-Keck, Z.Y.; Srivastava, M.; Kozak, C.A.; Caohuy, H.;
Biochem. J. 301, 835-845, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type:
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                   1-321 <TAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31;
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64.6%;
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ry, May 1993
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Pred. No. 2.7e-13;
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J. Biol. Chem. 263, 18657-18663, 1988
A;Title: Sedimentation equilibrium and
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A; Residues: 29-58;101-126;282-310 <AHN>
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A, Residues: 4-17;30-74;102-146;283-321 <TA3>
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A,Title: Structure and expression of cDNA for calphobindin II, a human placental coagula R,Reference number: JU0032; MUID:89380132; PMID:2528541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-673 <IWA>
A;Residues: 1-673 <IWA>
A;Cross-references: EMBL:D00510; NID:g219550; PIDN:BAA00400.1; PID:g219551
R;Crompton, M.R.; Owens, R.J.; Totty, N.F.; Moss, S.E.; Waterfield, M.D.; (EMBO J. 7, 21-27, 1988)
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 103-113;167-172, 'X',174-177;232-235, 'F',237-240;251-258;277-281;359-362, 'G'
A; Residues: 103-113;167-172, 'X',174-177;232-235, 'F',237-240;251-258, 277-281;359-362, 'G'
A; Note: eight calcium ions are bound in the presence of phospholipid
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A; Note: eight calcium ions are bound ions are bound ions a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Primary structure of the human, membrane-associated Ca(2+)-binding protein A;Reference number: S00263; MUID:88196081; PMID:3258820 A;Accession: S00263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;114-246/Domain: annexin repeat homology <AX3>;186-202/Region: endonexin fold #status predicted;250-321/Domain: annexin repeat homology <AX4>;250-321/Domain: annexin repeat homology <AX4>;261-277/Region: endonexin fold #status predicted;2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted;2/Modified site: phosphate (Thr) (covalent) (by protein kinase C) #status predic;9/Binding site: carbohydrate (Asn) (covalent) #status predicted;247/Binding site: carbohydrate (Asn) (covalent)
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                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-618,'D',620-673 <CRl>
A;Cross-references: EMBL:Y00097; NID:g35217; PIDN:CAA68286.1; PID:g35218
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                                                                                                                                                                                                                                                                                                          A;Accession: S1851
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Pred. No. 3.2e-13;
9; Mismatches 7
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S09020
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A;Residues: 1-225,'MK',228-554,'T',556-673 <SUE>
A;Cross-references: GB:J03578; NID:g179975; PIDN:AAA35656.1;
R;Yoshizaki, H.; Mizoguchi, T.; Arai, K.; Shiratsuchi, M.; Sh
J. Biochem. 107, 43-50, 1990
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R;Ahn, N.G.; Teller, D.C.; Bienkowski, M.J.; McMullen, B.A.; Lipkin, E.W.
J. Biol. Chem. 263, 18657-18663, 1988
A;Title: Sedimentation equilibrium analysis of five lipocortin-related ph
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A;Title: Identification and characterization of alpha-protein kinase A;Reference number: A53507; MUID:94153907; PMID:8110754
A;Accession: A53507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Hayashi, H.; Owada, M.K.; Sonobe, S.; Kakunaga,
J. Biol. Chem. 264, 17222-17230, 1989
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A; Residues: 10-25;69-75;136-151;192-207;209-220;300-306
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A; Residues: 90-108,'L',110-126;127,265-276;286-302;626-654 <AHN>
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A;Residues: 'X',473-480,'DY' <HYA>
C;Comment: This abundant cytosolic protein binds
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F;265-281/Region: endonexin fold
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34-50/Region: endonexin fold #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                    ;438-509/Domain:
                                                                                                                                                                                                                                                                                                                                                                  :449-465/Region:
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377-393/Region: endonexin fold #status
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                                                                                                                                                        Matches
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                                                                    373
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                                                                 RKAMKGLGTDEDTIIDIITHRSNVQRQQIRQTFKSHFGRDLMTDLKSE
                                                                                                         RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 48
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endonexin fold #status predicted
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endonexin fold #status predict
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endonexin fold
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                                                                                                                                                                                  72.3%;
                                                                                                                                                                                                                                                                                                                                                                                       homology <AX6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           #status predicted
                                                                                                                                                                                                                                                                                                                     #status predicted
                                                                                                                                                                                                                                                                                                                                                                    #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                      homology <AX5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nomology <AX4>
                                                                                                                                                                                                                                                                                                                                                 homology
                                                                                                                                                                                  Score 167; DB 1;
Pred. No. 7.4e-13;
                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              predicted
                                                                                                                                                                                                                                                                                                                                                    <AX7>
                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                        (in mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                duplication; endonexi
                                                                                                                                                                                                       Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anticoagulant pro
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Shidara, Y.; Ma
                                                                                                                                                                                                                                                             form) #status
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annexin VI - mouse
N;Alternate names: calcium-binding protein p68; calelectrin; calphobindin
C. Checies: Mus musculus (house mouse)
                                                                                                                                                                                          RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;176-248/Domain: annexin repeat homology <AX3>F;252-323/Domain: annexin repeat homology <AX4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: annexin VI; annexin repeat homology C; Keywords: calcium binding; phospholipid binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;93-164/Domain: annexin repeat homology <AX2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Cao, X.; Genge, B.R.; Wu, L.N.Y.; Buzzi, W.R.; Showman, R.M.; Wuthier, R.E. Biochem. Biophys. Res. Commun. 197, 556-561, 1993
A;Title: Characterization, cloning and expression of the 67-kDa annexin from chicken A;Reference number: JC2029; MUID:94092130; PMID:8267590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-671 < CAO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
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A;Residues: 1-36;37-53;54-64;65-81;82-105;106-116;117-137;138-150;151-157 <KOB>
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;601-671/Domain: annexin repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;525-597/Domain: annexin repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;436-507/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arch. Biochem. Biophys. 277, 203-210, 1990
A;Title: Purification, characterization, and partial sequence analysis of 32-kDa
A;Reference number: S09020; MUID:90165469; PMID:2137684
A;Accession: S09020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kobayashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               calcimedin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alternate names: 67K lipid-dependent Ca2+-binding protein (Species: Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: 809020;
Kobayashi, R.; Hidaka, H.; Tashima, Y.;
Kobayashi, R.; Hidaka, E.;
Tashima, Y.;
Tashima, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54-64/Domain: annexin repeat homology (fragment) <AXIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Species: Gallus gallus (chicken)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Date: 21-Nov-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                 RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE
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                                                                                                                                                                                                                                                               RKAMKGLGTDEGAIIEVLTQRSNAQRQQILKAYKAHYGRDLLADLKSE 418
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                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.9%;
70.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homology <AX7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homology <Ax6;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 166; DB 2;
Pred. No. 9.8e-13;
6; Mismatches 8
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Pred. No. 1.9e-13;
6; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       low affinity (Thr, Glu, Glu) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 671;
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R.Magendzo, K.; Shirvan, A.; Cultraro, C.; Srivastava, M.; Pol
J. Biol. Chem. 266, 3228-3232, 1991
A;Title: Alternative splicing of human synexin mRNA in brain,
A;Reference number: A39513; MUID:91131630; PMID:1825209
A;Molecule type: mRNA
A;Residues: 137-145,168-176 <MAG>
                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-145,168-488 <BUR>
                                                                                                                                                                                                                                                                       R;Burns, A.L.; Magendzo, K.; Shirvan, A.; Srivastava, M.; Rojas, E.; Alijani, M.R.; Polla Proc. Natl. Acad. Sci. U.S.A. 86, 3798-3802, 1989
A;Title: Calcium channel activity of purified human synexin and structure of the human synemics number. A32554; MUID:89264510; PMID:2542947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Contains: annexin VII, long form; annexin VII, short form C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 30-Sep-1992 #sequence_revision 26-Jan-1996 #text_change 22-Jun-1999 C;Accession: A54467; A32554; A39513; B39513 R;Shirvan, A; Srivastava, M; Wang, M.G.; Cultraro, C.; Magendzo, K.; McBr. Biochemistry 33, 6888-6901, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Divergent structure of the human synexin (annexin VII) A;Reference number: A54467; MUID:94264005; PMID:7515686 A;Accession: A54467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N; Alternate names: synexin
                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                 4;Residues: 1-488 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annexin VII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                               CTOSS-references: EMBL:J04543; NID:g338243; PIDN:AAA36616.1; PID:g338244; Magendzo, K.; Shirvan, A.; Cultraro, C.; Srivastava, M.; Pollard, H.B.; Burns,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;2/Modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;613-629/Region: endonexin fold #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;438-509/Domain: annexin repeat F;449-465/Region: endonexin fold
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                                                                                                                                                                                                                                                                  Accession: A32554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: acetylated amino end; calcium binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: annexin VI; annexin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X13460; NID:g53580; PIDN:CAA31808.1; PID:g53581 A;NOTE: the authors translated the codon GCC for residue 329 as Gly C;Comment: This abundant cytosolic protein binds to the inner surface of
                                                     Accession: A39513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Molecular cloning of murine p68, a Ca-binding protein A;Reference number: S01786; MUID:89030687; PMID:2972541
                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178-250/Domain: annexin repeat homology <AX3>
190-206/Region: endonexin fold #status predicted
254-325/Domain: annexin repeat homology <AX4>
265-281/Region: endonexin fold #status predicted
366-437/Domain: annexin repeat homology <AX5>
377-393/Region: endonexin fold #status predicted
438-509/Domain: annexin repeat homology <AX6>
449-465/Region: endonexin fold #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S01786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Moss, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 30-Sep-1989 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C;Accession: S01786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     538-554/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106-122/Region: endonexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-94/Domain: annexin repeat homology <AXl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2-673/Product: annexin VI #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.E.; Crompton, M.R.; Crumpton, Biochem. 177, 21-27, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         long form - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   site: acetylated amino end (Āla)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKAMKGIGTDEATIIDIVTHRSNAQRQQIRQTFKSHFGRDLMADLKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.0%;
nilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endonexin fold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annexin repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homology <AX8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 164; DB 1;
Pred. No. 1.7e-12;
8; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homology <AX7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (in mature form) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    duplication; endonexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                       cardiac,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K.; McBride,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and assignment to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                     and skeletal musc]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O.W.;
                                                                                                                                          A.L.
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C;Keywords: alternative splicing; calcium binding; calcium channel; duplication; endones F;1-488/Product: annexin VII, long form #status predicted <MAT> F;1-145,168-488/Product: annexin VII, short form #status predicted <MA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 10q21.1-10q21.2
A;Introns: 17/3; 87/1; 124/1; 145/3; 167/3; 202/2; 233/3; 271/3; 328/3; 385/3; 411/1; 4
C;Superfamily: annexin VII; annexin line binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 137-176 <MA2>
                                                                                                                                                                                                                                                     F;265-281/Region: endonexin fold #status predicted F;366-437/Domain: annexin repeat homology <AX5> F;377-393/Region: endonexin fold #status predicted F;377-393/Region: endonexin fold #status predicted F;438-509/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;343-415/Domain: annexin repeat F;355-371/Region: endonexin fold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;260-331/Domain: annexin repeat homology <AX2>
F;271-287/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;188-259/Domain: annexin repeat homology <AX1>
F;199-215/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        derstood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: cDNA cloning and tissue-specific regulation of A;Reference number: S65683; MUID:95331313; PMID:7607247 A;Accession: S65683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Fan, H.; Josic, D.; Lim, Y.P.; Reutter, W. Bur. J. Biochem. 230, 741-751, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: calcium-binding protein 65/67
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            annexin VI -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       뭉
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: GDB:ANX7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: B39513
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                                                                                                                                                                                                                                                                                                                                                                                         F;190-206/Region: endonexin fold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X86086; NID:g763180; PIDN:CAA60040.1; PID:g763181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-673 <FAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :Comment:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;430-446/Region:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;95-166/Domain: annexin repeat homology <AX2>;106-122/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-94/Domain: annexin repeat homology <AX1>
34-50/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily: annexin VI; annexin repeat homology; Keywords: acetylated amino end; calcium binding; 2-673/Product: annexin VI #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
Accession: S65683; S52844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                      106-122/Region: endonexin
178-250/Domain: annexin re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 RKAMKGFGTDEQAIVDVVANRSNDQRQKIKAAFKTSYGKDLIKDLKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The long form of annexin VII is more prevalent in brain, heart, and skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  annexin repeat endonexin fold
                                                                                                                                                                                                                           annexin repeat endonexin fold
                                                                                                                                                                                                                                                                                                                                                                                                                         annexin repeat
                                                                                                                                                                          endonexin fold
                                                                                                                                                                                                      annexin repeat
                                                                                      endonexin fold #status predicted
acetylated amino end (Ala) (in mature form) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.6%; Score 163; DB 1; 64.6%; Pred. No. 1.6e-12; tive 10; Mismatches 7
  70.1%;
64.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #status predicted homology <AX4>
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                                                                                                                                                                                                                                                                                                                                                                                            #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                         homology <AX3>
                                                                                                                                                                                                      homology
                                                                                                                                                                                                                           #status predicted
                                                                                                                                                homology
                                                                                                                                                                    #status predicted
  Score 162; DB 1;
Pred. No. 3.1e-12;
                                                                                                                                                                                                    <AX7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endonexin fold; membrane-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 488;
                            Length 673
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Job time

Search completed: April

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N;Alternate names: calcyclin-associated protein peptide, CA (;Species: Bos primigenius taurus (cattle) (cpate: 31-Mar-1993 #text ch (;Date: 31-Mar-1993 #tequence_revision 31-Mar-1993 #text ch (;Accession: A42113; A42909; B42909; C42909; D42909 | R;Towle, C.A.; Treadwell, B.V. J. Biol. Chem. 267, 5416-5423, 1992 | A;Reference number: A42113; MUID:92184796; PMID:1372001 | A;Reference number: A42113; MUID:92184796; PMID:1372001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M82802; NID:g162673; PIDN:AAA30379, 1; PID:g162674
A;Note: the authors did not translate the codon GAC for residue 503
R;Mizutani, A.; Usuda, N.; Tokumitsu, H.; Minami, H.; Yasui, K.; Kobayashı
J. Biol. Chem. 267, 13498-13504, 1992
A;Title: CAP-50, a newly identified annexin, localizes in nuclei of cultural, Reference number: A42909; MUID:92317074; PMID:1618851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                      F;432-503/Domain: annexin repeat homology <AX4>
F;443-459/Region: endonexin fold #status predicted
F;59,111/Binding site: carbohydrate (Asn) (covalent
                                           Ş
                                                                                                                                                                                                                                                                                                                F;284-300/Region:
                                                                                                                                                                                                                                                                                                                                                            F;201-272/Domain: annexin repeat F;212-228/Region: endonexin fold
                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: annexin VII; annexin repeat homology C; Keywords: calcium binding; duplication; endonexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 19/1; 56/2
A;Note: the list of introns is incomplete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     derstood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: sequence modified after extraction from NCBI backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 213-223, 'X', '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A42909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-503 <TOW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: A42113
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  문
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                                                                                                                                                                                                                                                                                          F;356-428/Domain:
                                                                                                                                                                                                                                                                                                                                           F;273-344/Domain:
                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comment: Annexins undergo reversible, calcium-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                           Query Match
                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373
  208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31;
                                                                                               31;
                                         1 RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 48
                                                                                                                       Similarity
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RKAMKGFGTDEQAIIDCLGSRSNKQRQQILLSFKTAYGKDLIKDLKSE
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                                                                                                                     68.8%;
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                                                                                                                                                                                                                                                                                                                   #status predicted
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                                                                                                                       Score 159; DB 1;
Pred. No. 5.3e-12;
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1 231 100.0 319 1 US-08-125-746-1 Sequence 1, Appli 323 100.0 320 1 US-08-125-746-3 Sequence 1, Appli 323 100.0 320 6 5225537-4 Sequence 2, Appli 6 231 100.0 327 4 US-09-324-096A-2 Sequence 2, Appli 6 231 100.0 327 4 US-09-324-096A-6 Sequence 4, Appli 100.0 327 4 US-09-324-096A-6 Sequence 2, Appli 8 100.0 327 4 US-09-324-096A-6 Sequence 2, Appli 9 100.0 327 4 US-09-324-096A-6 Sequence 3, Appli 100.0 327 4 US-09-324-096A-6 Sequence 2, Appli 100.0 327 4 US-08-948-276-3 Sequence 2, Appli 100.0 327 4 US-08-326-136-1 Sequence 2, Appli 100.0 327 4 US-08-326-136-1 Sequence 1, Appli 110.0 324 4 US-08-326-136-1 Sequence 2, Appli 110.0 324 4 US-08-326-136-1 Sequence 3, Appli 110.0 324 4 US-08-3276-6 Sequence 3, Appli 110.0 324 4 US-08-3276-6 Sequence 3, Appli 110.0 324 4 US-08-328-276-6 Sequence 3, Appli 110.0 324 4 US-08-328-276-6 Sequence 3, Appli 110.0 324 4 US-09-325-32A-65 Sequence 6, Appli 110.0 324 3 US-08-328-328-65 Sequence 6, Appli 110.0 328-328-328-5 Sequence 6, Appli 110.0 328-328-65 Sequence 2, Appli 110.0 328-328-65 Sequence 2, Appli 110.0 328-328-65 Sequence 2, Appli 110.0 328-328-32	SUMMARIES Result Query No. Score Match Length DB ID Description	pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Database: Issued Patents AA:* 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:* 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:* 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:* 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:* 5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:* 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Searched: 30911 seque, Javanova Forente 389414 Total number of hits satisfying chosen parameters: 389414	LOSUM62 apop 10.0 ,	Title: US-09-787-923-2_COPY_25_72 Perfect score: 231 sequence: 1 RKAMKGLGTDEESILTLLTSISAAFKTLFGRDLLDDLKSE 48	OM protein - protein search, using sw model Run on: April 8, 2004, 11:55:51; Search time 23 Seconds (without alignments) 107.741 Million cell updates/sec	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
APPLICATION NUMBER: US/08/125,746 FILING DATE: 24-SEP-1993 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/807,623 FILING DATE: 13-DEC-1991 PRIOR APPLICATION NUMBER: JP 037227/1987 APPLICATION NUMBER: JP 037227/1987 PRIOR APPLICATION NUMBER: JP 184428/1987 PRIOR APPLICATION NUMBER: JP 184428/1987 PRIOR APPLICATION NUMBER: JP 184428/1987 APPLICATION NUMBER: JP 184428/1987 APPLICATION NUMBER: JP 184428/1987 APPLICATION NUMBER: 3-JUL-1987 APPLICATION NUMBER: 24,618 REGISTRATION NUMBER: 24,618 REGISTRATION NUMBER: 24,618 REFERENCE/DOCKET NUMBER: 80-074-0 DIV TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 413-3000 TELEFAX: 248855 OPAT UR INFORMATION POR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 319 amino acids TYPE: amino acids TOPOLOGY: Unknown MOLECULE TYPE: protein	COMPUTER REALIZED CONT. MEDIUM TYPE: Flopy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 COMPUTER: TOATTON DATA.		APPLICANT: APPLICANT: APPLICANT: APPLICANT: SUDA, MAKOTO APPLICANT: SUDA, MAKOTO ITITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDLESS: ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSE: P.C. ADDRESSE: P.C. ATTICLE ATTICLE. ATTICLE ATTICLE.	; sequence 1, Application (); patent No. 5591613 ; GENERAL INFORMATION: ; APPLICANT: SAINO, YUSHI ; SETICANT: AFFO	146.	ALIGNMENTS	675 4 819 4	52 22.5 1037 4 US-09-543-681A-7677 52 22.5 1038 4 US-09-543-681A-5641 52 22.5 1398 4 US-09-343-47A-76 52 22.5 3788 4 US-09-36-47A-76 52 22.3 342 4 US-09-107-532A-5664	52.5 22.9 52.5 22.7 52.22.5 52.5 22.7	53.5 23.2 297 4 US-09-543-681A-6240 53.5 23.2 450 4 US-09-489-039A-13998 53.5 23.2 608 4 US-08-843-572E-2 53.2 9 1996 2 US-08-804-227C-9 53 22.9 1996 2 US-08-804-198-3 53 22.9 1996 2 US-08-804-227C-14

Sequence 6240,
Sequence 13998
Sequence 2, Ap
Sequence 9, Ap
Sequence 8, Ap
Sequence 8, Ap
Sequence 8, Ap
Sequence 9827,
Sequence 9827,
Sequence 9853,
Sequence 34, Ap
Sequence 76, 77,
Sequence 76, 77,
Sequence 76, 77,
Sequence 76, 78,
Sequence 76, 78,
Sequence 76, 78,
Sequence 76, 78,
Sequence 5641,
Sequence 5642,
Sequence 5643,
Sequence 5644,
Sequence 5644,

Sequence

5641, 76, P 5664 8, A 5342

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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 80 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/807,623
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             FILING DATE: 23-JUL-1987
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5591633
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 20-FEB-1987 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 24-SEP-19
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                              TELEPHONE: (703)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                          NAME: Oblon, No. 5591633man F. REGISTRATION NUMBER: 24,618
                                                                               ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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les 48; Conservative
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       25
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CANT: SAINO, YUSHI
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                       RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 48
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                                                                                                                                                                                                                                                               (703) 413-3000
                                                                                                                                          protein
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DEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 72
                                                                            100.0%;
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                                                                       Score 231; DB 1;
Pred. No. 4.2e-26;
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                                                            Mismatches
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                                                                                        Length 320;
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RESULT 3

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US-09-324-096A-2
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US-09-324-096A-2
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          Matches
                                         Query Match
                                                                                                                                            SOFTWARE: PatentIn
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FOSTER, DONALD TITLE OF INVENTION: METHO: PHOSPHOLIPID-BINDING PROTEINS NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-948-276-1
                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                sequence 2, Application US/09324096A
Patent No. 6323313
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Best Local Similarity
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                                                                                      LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/324,096A
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APPLICANT: Ernst, Joel D.
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UCSF97-113
                                                                                                                                                                             NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                  FILE REFERENCE: UOFW-1-13841
                                                                                                                                                                                                                                                                   APPLICANT: Tait, Jonathan APPLICANT: Brown, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                   PHICANT: Brown, David
TLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 29-DEC-1989
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          48;
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        Conservative
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                                                                                                                                                            version 3.0
100.0%; Score 231; DB 4; 100.0%; Pred. No. 4.4e-26; tive 0; Mismatches 0;
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100.0%; Pred. No. 4.2e-26;
tive 0; Mismatches 0;
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                                 Length 327;
Indels
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RESULT 6
US-09-324-096A-4
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APPLICANT: Tait, Jonathan
APPLICANT: Brown, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09324096A Patent No. 6323313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/324,096A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 6, Application US/09324096A Patent No. 6323313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Brown, David
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
FILE REFERENCE: UCFW-1-13841
CURRENT APPLICATION NUMBER: US/09/324,096A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 12
                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                Sequence 2, Application US/08948276 Patent No. 6511829
                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tait, Jonathan
APPLICANT: Brown, David
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
FILE REFERENCE: UOFW-1-13841
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                        APPLICANT: Ernst, Joel D.
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REPERENCE: UCSF97-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 327
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                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE
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                                                                                                                                                                                                                                                                                                                                     100.0%; Score 231; DB 4;
100.0%; Pred. No. 4.4e-26;
tive 0; Mismatches 0;
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GENERAL INFORMATION:
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Best Local Similarity 87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ernst, Joel D.
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UCSF97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Applic Patent No. 5849600
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                                                                                                                                                                                                ZIP: 02110-2804
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC-DOS/MS-DOS
COPTUNING SYSTEM: PC-DOS/MS-DOS
COPTUNING: PC-POIS MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nixon, Ralph
APPLICANT: Honda, Toshiyuki
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                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                          ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T.
                                                                                                                                                                    SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 11-NOV-1993 CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                    CITY:
                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                              COUNTRY:
                                          REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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79.2%;
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                                                                                                                                                                                     Release #1.0, Version #1.30
                                                                                                                                                       US/08/149,975A
                                                             30,162
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Pred. No. 1.3e-20;
                                                04843/016001
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..5e-22;
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TELEX: 200154
INFORMATION FOR SEQ ID NO:

TELEFAX:

617/542-8906

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US-08-526-136-14
                                                         Matches
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                                                                                                                                                                                                   TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Towle, Christine A.
TITLE OF INVENTION: ANNEXIN XI
                                                                                                                                                                                                                                            NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00°
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette,
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                                                                       Local
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                                                                                                                                             TYPE: amino acid
STRANDEDNESS: N/A
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                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: Februa APPLICATION NUMBER:
                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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1 RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 48
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                                                                    Similarity
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                                                     Conservative
                                                                                                                                                                                                                                (617) 542-8906
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SYSTEM: IBM P.C. DOS (Version 3.30)
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                                                                  74.9%;
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                                                                                                                                                                                                      14:
                                               Score 173; DB 3; ]
Pred. No. 1.7e-17;
6; Mismatches 8;
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Pred. No. 1.3e-20;
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                                                                           Length 319;
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US-08-526-136-13
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US-08-948-276-4
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                                                  INFORMATION FOR SEQ ID NO:
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Best Local Similarity
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                                                                                                  REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEO ID NOS: 6 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ernst, Joel D.
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UCSP97-113
                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2 Model 50Z or 55S
OPERATING SYSTEM: IBM P.C. DOS (Ver
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
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ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER. READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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                 ENGTH:
                                                                                    TELEFAX:
                                                                                                                                                                              NAME:
                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/214,036
                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 RKAMKGLGTDEDATISVLAYRNTAQRQEIRTAYKSTIGRDLIDDLKSE 73
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                                                                                                                                                                        Clark, Paul T.
amino acid
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                                                                                    (617) 542-8906
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ary 13, 1992
                                                                                                                               30,162
BER: 00786/099001
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Pred. No. 1.3e-16;
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; Sequence 2, Application US/08526136
; Patent No. 6107089
; GENERAL INFORMATION:
APPLICANT: Towle, Christine A. et
TITLE OF INVENTION: ANNEXIN XI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
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Sequence 4, Application US/08526136 Patent No. 6107089 GENERAL INFORMATION:
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                                                                                                                                                                                                               Query Match 68.8%;
Best Local Similarity 64.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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TOPOLOGY: N/A
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TOPOLOGY: N/A
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                                                                                                                         208 RKAMKGFGTDEQAIIDCLGSRSNKQRQQILLSFKTAYGKDLIKDLKSE 255
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Similarity 64.6%;
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Pred. No. 8.2e-16;
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Best Local Similarity
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                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT IMFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Towle, Christine A. TITLE OF INVENTION: ANNEXIN XI NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                         NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00
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STATE: Massa
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210 RKAMKGFGTDEQAIIDCLGSRSNKQRQQILLSFKTAYGKDLIKDLKSE 257
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                                                                                                                                                                                      amino acid
                   RKAMKGLGTDEESILTLLITSRSNAQRQEISAAFKTLFGRDLLDDLKSE 48
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Pred. No. 3.6e-15;
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1 RKAMKGLGTDEESILTLLTS....
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US-10-007-761-72
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Sequence 731, Appl
Sequence 1, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 6, Appli
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Sequence 16, Appli
Sequence 1062, Appli
Sequence 1664, Appli
Sequence 1664, Appli
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ALIGNMENTS	US-10-316-253-262 US-10-316-253-300 US-09-925-301-897 US-09-974-298-91 US-10-097-340-6 US-10-097-340-6 US-10-104-047-2800 US-09-764-853-615 US-09-764-853-615 US-09-974-287-2 US-09-919-172-39 US-09-919-172-39 US-09-925-301-888 US-10-242-747-110 US-09-925-301-1467 US-10-424-599-213299 US-09-925-301-1467 US-10-424-599-213299 US-10-424-599-279847 US-10-424-599-279848 US-10-424-599-21908 US-10-424-599-279848 US-10-424-599-279848 US-10-393-840-52 US-10-393-840-52 US-10-393-840-52 US-10-393-840-118 US-10-393-840-52 US-10-393-840-52	US-10-424-599-2
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RESULT 1
US-09-925-302-731
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US-10-007-761-72
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                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 731
LENGTH: 208
TYPE: PRT
GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: Peptides for Activation and Inhibition
                                                         Sequence 72, Application US/10007761 Publication No. US20020150984A1
                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR PILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 896
                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                    28
                                                                                                                                                                                                                                                                48;
                                                                                                                                                                                                                     1 RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 48
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                    RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 75
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                              Score 231; DB 9;
Pred. No. 1.8e-24;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                          Length 208;
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Gaps

TITLE OF INVENTION:

of delta-PKC

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US-09-970-969-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-007-761-72
                                                         SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 327
                                                                                                                                                                                                                                                                 Sequence 2, Application US/09970969 Patent No. US20020103341A1
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.2 SEQ ID NO 1
09-970-969-2
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                                                                                                                                  CURRENT FILING DATE: 2001-10-03
                                                                                                                                                                       APPLICANT: Brown, David S.
TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites
FILE REFERENCE: uofw-1-13841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
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                                                                                                                 NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                           APPLICANT: Tait, Jonathan F. APPLICANT: Brown, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/424,232
CURRENT FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 60/60/376,052
                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2002-04-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 58600-8208.US00
CURRENT APPLICATION NUMBER: US/10/007,761
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/262,060
PRIOR FILING DATE: 2001-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bogdanov, Alexei APPLICANT: Schellenberger,
                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLICANT: Schellenberger, Eyk
PPLICANT: Petrovsky, Alexander
PPLICANT: Josephson, Lee
ITLE OF INVENTION: In vivo Imaging of Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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No. US20040022731A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 231; DB 16;
Pred. No. 3.1e-24;
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CURRENT APPLICATION NUMBER: US/09/970,969
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 4
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-970-969-4
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Best Local S
                                                 Sequence 3, Application US/10080370 Publication No. US20030166532A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 6
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09970969 Patent No. US20020103341A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                APPLICANT: Allison, TITLE OF INVENTION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/970,969
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Brown, David S.
TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites
FILE REFERENCE: uofw-1-13841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tait, Jonathan F. APPLICANT: Brown, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tait, Jonathan F.
APPLICANT: Brown, David S.
TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation
FILE REFERENCE: unofw-1-13841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                               32 RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE
                                                                                                                                                                                                      1 RKAMKGLGTDEESILTLLISRSNAQRQEISAAFKTLFGRDLLDDLKSE 48
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                                                                                                                                                                                                                                                         Similarity 100.
48; Conservative
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Anthony
Modified Annexin Proteins and Methods for Preventing Thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 231; DB 9; 100.0%; Pred. No. 3.2e-24;
                                                                                                                                                                                                                                                     100.0%; Score 231; DB 9;
100.0%; Pred. No. 3.2e-24;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                         Length 327;
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                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Allison, Anthony
TITLE OF INVENTION: Modified Annexin Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/10080370 Publication No. US20030166532A1
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Matches 38; Conservative
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                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (351). (351)
COTHER INFORMATION: The 'Xaa' at location 351 stands for Lys, Asn, Arg, Ser, Thr, Ile
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
OTHER INFORMATION: modified annexin gene
NAME/KEY: misc feature
LOCATION: (45). (45)
OTHER INFORMATION: n = a, c, g, or t
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CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/270,402
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/332,582
PRIOR FILING DATE: 2001-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/080,370 CURRENT FILING DATE: 2002-02-21 PRIOR APPLICATION NUMBER: 60/270,402 PRIOR FILING DATE: 2001-02-21 PRIOR APPLICATION NUMBER: 60/332,582 PRIOR FILING DATE: 2001-11-21 NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
                                                                                                                NAME/KEY: misc_feature LOCATION: (334)..(334)..(334) COTHER INFORMATION: The 'Xaa' at location 334 stands for Lys, Asn, Arg, Ser, Thr, Ile OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
                                                                                                        LOCATION: (1051)..(1053)
OTHER INFORMATION: n = a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial sequence
                                                                                                                                                                                             NAME/KEY: misc feature LOCATION: (1000)..(100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature LOCATION: (15)..(15)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: The 'Xaa' at location 15 stands for Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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TYPE: PRT
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      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SURR.90
                       84.0%;
79.2%;
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Score 194; DB 14;
Pred. No. 1.4e-18;
7; Mismatches 3;
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Pred. No. 5.6e-19;
7; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Methods for Preventing Thrombosis
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    Indels
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                                                                                                                                                      RESULT 10
US-09-925-301-1062
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
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                                                                                                                  Sequence 1062, Application US/09925301
                                                                                                                                                                                                                                                                                                                                                                                                           SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 321
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/323,580 PRIOR FILING DATE: 2001-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/097,340 CURRENT FILING DATE: 2002-03-14 PRIOR APPLICATION NUMBER: 60/276,025 PRIOR FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Nucleic Acid Molecules and Proteins TITLE OF INVENTION: Assessment, Prevention, and Therapy FILE REFERENCE: MRI-030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-08-10
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FILING DATE: 2001-09-26
APPLICATION NUMBER: 60/276,026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/311,732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-03-14
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Karen GLATT
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Shubhangi KAMATKAR
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Robert C. BAST, Jr.
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66.7%;
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Pred. No. 3.8e-15;
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RESULT 11
US-10-114-270-160
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SEQ ID NO 1062
LENGTH: 324
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ORGANISM: Homo sapiens
-09-925-301-1062
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PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
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APPLICANT: Rothenberg, Mark E.
TITLE OF INVENTION: No. US20040030110A1el Proteins and Nucleic Acids Encoding
FILE REFERENCE: 21402-322C
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                                                                                  PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906
                                                                                                                                     PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/114,270
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/281,086
                                PRIOR APPLICATION NUMBER: 60/282,020 PRIOR FILING DATE: 2001-04-06
                                                                  PRIOR FILING DATE: 2001-04-05
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FILING DATE:
                APPLICATION NUMBER: 60/282,930
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Miller, Charles E.
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Edinger, Shlomit R.
Stone, David J.
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Liu, Ziaohong
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Shimkets, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gorman, Linda
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2001-04-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catherine E.
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; ORGANISM: Homo sapiens
US-10-114-270-160
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SEQ ID NO 1664
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Best Local (
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                                                          APPLICANT: Jensen, Roderick V.
APPLICANT: Gullans, Steven R.
APPLICANT: Bueno, Raphael
TITLE OF INVENTION: Diagnostic and Prognostic
FILE REFERENCE: B00801/70265 (JRV/JAV)
CURRENT APPLICATION NUMBER: US/10/236,031B
CURRENT FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/317,389
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APPLICANT: Steve Ruber
PRIOR FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/407,431
PRIOR FILING DATE: 2002-08-30
                                                                                                                                                                                                                                  APPLICANT: Gordon, Gavin J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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FILING DATE: 2001-04-12
APPLICATION NUMBER: 60/283,710
FILING DATE: 2001-04-13
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l Similarity 66.7%;
32; Conservative
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Pred. No. 9.9e-15;
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; NAME/KEY: SITE
; LOCATION: (66)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-297-479
                                                                                                                                                                                                                                                                                                                                                 US-10-205-823-34
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US-09-925-297-479
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PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 479
                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         Sequence 34, Application US/10205823
Publication No. US20030108963A1
                                                                                         APPLICANT:
APPLICANT:
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Best Local Similarity
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APPLICANT:
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 479, Application US/09925297
Patent No. US20020081659A1
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APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                     39 QKAIRGIGTDEKMLISILTERSNAQRQXIVKEYQAAYGKELKDDLKGD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 48
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                                                                                                                                         Monahan, John E.
Endege, Wilson O.
Gamnavarapu, Manjula
Gorbatcheva, Bella
Hoersch, Sebastian
Kamatkar, Shubhangi
                                                                                       Zhao, Xumei
                                                                                                           Wonsey, Angela M.
Glatt, Karen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.6%; Score 133; DB 9
47.9%; Pred. No. 1e-10;
tive 15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 15; Length 327;
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RRENT APPLICATION NUMBER: US/10/205,823

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Search completed: April 8, 2004, 12:00:07 Job time : 41 secs
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                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 323
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                           Matches
                                                                                                                                                                                               Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2002-07-25
                                                                             28 OKAIRGIGTDEKMLISILTERSNAOROLIVKEYOAAYGKELKDDLKGD 75
                                                                                                                                                                           23;
                                                                                                                        1 RKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSE 48
                                                                                                                                                                                               Similarity
                                                                                                                                                                           Conservative
                                                                                                                                                                    56.7%; Score 131; DB 14;
47.9%; Pred. No. 4.9e-10;
tive 15; Mismatches 10;
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Gaps

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Sequence 6, Appli
Sequence 110, Appl
Sequence 110, Appl
Sequence 110, Appl
Sequence 2250, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 300, Appl
Sequence 5717, Appl
Sequence 5717, Appl
Sequence 5717, Appl
Sequence 65950, Appl
Sequence 52117, Appl
Sequence 5210, Appl
Sequence 52360, Appl
Sequence 52270, Appl
Sequence 52360, Appl
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Sequence 52270, Appl
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Sequence 52270,
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Sequence 186704,
Sequence 2936, Ap
Sequence 201914,
Sequence 223868,
             Sequence 91,
US-09-974-298-91

US-09-764-881-110

US-09-764-833-615

US-10-097-340-8

US-10-097-340-8

US-10-09-764-833-615

US-10-204-247-110

US-09-925-301-888

US-10-242-747-110

US-09-925-301-888

US-10-242-747-250

US-09-925-301-888

US-10-36-493-5695

US-09-9172-39

US-09-917-3944

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US-10-264-049-2936
US-10-424-599-201914
US-10-424-599-223868
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Sequence 4, Appli
Sequence 6, Appli
Sequence 3, Appli
Sequence 131, App
Sequence 10, App
Sequence 160, App
Sequence 160, App
Sequence 180, App
Sequence 180, App
Sequence 18, Appl
Sequence 24, Appl
Sequence 24, Appl
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Sequence 1, Appli
                                                                                                                                                                  2004, 08:05:00 ; Search time 46 Seconds (without alignments) 1820.256 Million cell updates/sec
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1600
1 MAQVLRGTVTDFPGFDERAD......KGDTSGDYKKALLLLCGEDD 320
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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           GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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6 US-10-424-233-1
US-09-970-969-2
US-09-970-969-6
4 US-10-080-370-3
4 US-10-080-370-6
US-09-925-302-731
4 US-10-097-340-10
US-09-925-301-1062
US-09-925-301-1062
US-10-114-270-160
5 US-10-114-270-160
5 US-10-316-334
4 US-10-336-031B-18
7 US-10-3316-334
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Maximum Match 100%
Listing first 100 summaries
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Sequence 1467, Ap
Sequence 243530,
Sequence 30160, A
Sequence 952, App
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                                                                                                                     sequence 63, Appl
Sequence 115, App
Sequence 3937, Ap
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             Sequence 71353, A
Sequence 198302,
Sequence 279848,
                                                                                                      Sequence 160681,
Sequence 63, App
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APPLICANT: Mochly-Rosen, Daria
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: of dalta-PKC
FILE REFERENCE: 58600-8208.US00
CURRENT APPLICATION NUMBER: US/10/007,761
CURRENT PILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/262,060
PRIOR FILING DATE: 2001-01-18
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FASELSEQ for Windows Version 4.0
5 US-10-393-840-951

2 US-10-425-114-71353

2 US-10-424-599-279848

US-09-925-301-1467

2 US-10-424-599-279848

US-09-925-301-1467

2 US-10-424-599-245330

5 US-10-033-840-952

2 US-10-393-840-952

2 US-10-393-840-953

3 US-10-393-840-155

5 US-10-393-840-155

5 US-10-264-049-3937
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                                                                                                                                                                                                                                                       Sequence 72, Application US/10007761 Publication No. US20020150984A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 320; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-761-72
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Sequence 1, Application US/10424232; Publication No. US20040022731A1; GENERAL INFORMATION:
APPLICANT: Bogdanov, Alexei

RESULT 2 US-10-424-232-1

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VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVGRSEIDLFNIRKEFRKNFATSLYSMI 300
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parente No. US2020103341A1
general No. US2020103341A1
general INFORMATION:
APPLICANT: Tait, Jonathan F.
APPLICANT: From David S.
TITLE OF INVENTION: Annexth Derivatives with Endogenous Chelation Sites
FILE REFERENCE: uofw-1-13841
CURRENT APPLICATION NUMBER: US/09/970,969
CURRENT PILIG DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 6
SOSTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                            100.0%; Score 1600; DB 16;
100.0%; Pred. No. 2.6e-139;
Live 0; Mismatches 0;
APPLICANT: Schellenberger, Eyk
APPLICANT: Petrovsky, Alexander
APPLICANT: JGsephson, Lee
TITLE OF INVENTION: In vivo Imaging of Apoptosis
FILE REPERROKE: 00786-549001
CURRENT APPLICATION NUMBER: US/10/424,232
CURRENT FILING DATE: 2003-04-25
PRIOR PLILNG DATE: 2003-04-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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Best Local Similarity 99.7
Matches 319; Conservative
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Matches 320; Conservative
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CRGANISM: Homo sapiens
US-09-970-969-2
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ORGANISM: Homo sapiens
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Gaps

KGDTSGDYKKALLLLCGEDD 320

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l, Application US/09970969 US20020103341A1

: Tait, Jonathan F.

FORMATION:

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APPLICANT: Allison, Anthony
TITLE OF INVENTION: Modified Annexin Proteins and Methods for Preventing Thrombosis
FILE REFERENCE: SURR. 90
CURRENT APPLICATION NUMBER: US/10/080,370
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/270,402
PRIOR PLING DATE: 2001-02-21
PRIOR PLING DATE: 2001-02-21
PRIOR PLING DATE: 2001-11-21
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              APPLICANT: Tait, Jonathan F. APPLICANT: Tait, Jonathan F. APPLICANT: Brown, David S. TITLE OF INVENTION: Annual Derivatives with Endogenous Chelation Sites FILE REFERENCE: uofw-1-13841 CURRENT APPLICATION NUMBER: US/09/970,969 CURRENT APPLICATION NUMBER: 10:03 NUMBER OF SEQ ID NOS: 6 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 2.0 LENGTH: 327 TYPE: PRT
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2.2e-138;
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99.7%; Pred. No. 2.2¢
:ive 0; Mismatches
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
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Matches 319; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-970-969-6
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1. FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
                                  8 FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
                                                                                                              1 ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF 180
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INVENTION: Annexin Derivatives with Endogenous Chelation Sites
RRENCE: uofw-1-13841
RPDLICATION NUMBER: US/09/970,969
FILING DATE: 2001-10-03
Patentin Ver. 2,0
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Length 327;

99.4%; Score 1590; DB 9; 99,7%; Pred. No. 2.2e-138; iive 0; Mismatches 1;

119; Conservative

Similarity

1: Homo sapiens

6, Application US/09970969 . US20020103341A1

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125 IKQVYEBEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGE 184
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                                                                                                                                                                                                                                                                    244
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63
                                                                          LLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA
                                                                                                                                                                                                                                                                                              197 LKWGIDEEKFITILGTRSVSHLRRVFDKYMTISGFQIEETIDRETSGNLENLLLAVVKSI
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR PLICATION NUMBER: 60/124,270
PRIOR PLICAGO DATE: 1999-00-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Pate: 110 Ver. 2.0
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// Patent No. US20320044941A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGDYKKALLLCGGEDD 333
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; ORGANISM: Homb sapiens
US-09-925-302-731
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US-10-097-340-10
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OTHER INFORMATION: The 'Xaa' at location 334 stands for Lys, Asn, Arg, Ser, Thr, Ile OTHER INFORMATION: The 'Xaa' at location 334 stands for Lys, Asn, Arg, Ser, Thr, Ile OTHER INFORMATION: Tyr, Trp, Cys, or Phe.

NAME/KEY: misc feature
LOCATION: (351). (351)

OTHER INFORMATION: The 'Xaa' at location 351 stands for Lys, Asn, Arg, Ser, Thr, Ile OTHER INFORMATION: The 'Cys, or Phe.

OTHER INFORMATION: Tyr, Trp, Cys, or Phe.

OTHER INFORMATION: Modified annexin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Alison, Anthony
TITLE OF INVENTION: Modified Annexin Proteins and Methods for Preventing Thrombosis
FILE REPERENCE: SURF. 30
CURRENT APPLICATION NUMBER: US/10/080,370
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/270,402
PRIOR FILING DATE: 2001-02-21
PRIOR FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 9
SOFFWARE: Patentin version 3.1
SEQ ID NO 6
LENTH: 669
                                                                                                                                           183 LKWGTDEEKFITILGTRSVSHLRRVFDKYMTISGFQIEETIDRETSGNLENLLAAVVKSI 242
                                                                                                                                                                                                                                                                                                                                         243 RSIPAYLAETLYYAMKGAGTDDHTLIRVIVSRSEIDLFNIRKEFRKNFATSLYSMIKGDT 302
                          LLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA 124
                                                                                                                   125 IKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGE
                                                                                                                                                                                                                                                                                                            245 RSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDT
                                                                                                                                                                                                                 LKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSI
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OTHER INCRNATION: The 'Xaa' at location 15 stands for Ser.NAME/KEY: misc feature
LOCATION: (334)...(334)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.7%; Score 1451.5; DB 14; Lengt]
91.5%; Pred. No. 3.9e-125;
tive 12; Mismatches 14; Indels
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OTHER INFORMATION: n = a, c, g, or
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Publication No. US20030166532A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                        305 SGDYKKALLLLC-GEDD .320
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OTHER INFORMATION: n = a, c,
NAME/KEY: misc_feature
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OTHER INFORMATION: n = a, c,
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Best Local Similarity 91.5%
Matches 290; Conservative
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LOCATION: (1051)..(105:
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US-10-080-370-6
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Manjula GANNAVARAPU Sebastian HOERSCH Shubhangi KAMATKAR Steve G. KOVATS Rachel E. MEYERS Michael MORRISEY Peter OLANUT

Gordon B. MILLS Robert C. BAST, Jr

Karen LU

Ami SEN Peter VEIBY

Rosemarie SCHMANDT Xumei ZHAO Karen GLATT

APPLICATION NUMBER: US/10/097,340

ERENCE: MRI-030

FILING DATE: 2002-03-14
LING DATE: 2001-03-14
LING DATE: 2001-03-14
LING DATE: 2001-03-14
LING DATE: 2001-03-26
LING DATE: 2001-03-26
PLICATION NUMBER: 60/276,026
LING DATE: 2001-03-14
PLICATION NUMBER: 60/324,967
LING DATE: 2001/09/26
PLICATION NUMBER: 60/311,732
LING DATE: 2001-03-10
PLICATION NUMBER: 60/311,732
LING DATE: 2001-03-10
PLICATION NUMBER: 60/312,102
PLICATION NUMBER: 60/312,102
PLICATION NUMBER: 60/312,102
PLICATION NUMBER: 60/312,102

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71 DDLKSELSGNFEQVIVGMMTPTVLYDVQELRRAMKGAGTDEGCLIEILASRTPEEIRRIS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 DDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG 306
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Sequence 1062, Application US/09925301
Fatent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION:
FILE REFERENCE: PA106
CURRENT FAPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: ECT/US00/05882
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77; Indels
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Best Local Similarity 58.6%; Pred. No. 1.1e-77;
Matches 184; Conservative 53; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 160, Application US/10114270; Publication No. US20040030110A1; GENERAL INFORMATION:
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Smithson, Glenda
Burgess, Catherine E.
Gerlach, Valerie
Padigaru, Muralichara
Shimkets, Richard A.
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Spytek, Kimberly A.
Patturajan, Meera
Liu, Ziaohong
Gusev, Vladimir Y.
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APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles E.
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Gorman, Linda
Shenoy, Suresh G.
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311 DYRKVLLVLCGGDD 324
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Vernet, Corine
                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1062
LENGTH: 324
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 QVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 QTYQQQYGRSLEDDIRSDTSFMFQRVLVSLSAGGRDEGNYLDDALVRQDAQDLYEAGEKK 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 KSAYFAEKLYKSMKGLGTDDNTLIRVMVSRAEIDMLDIRAHFKRLYGKSLYSFIKGDTSG 307
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88 WGTDEVKFLTVLCSRNRNHLLHVFDEYKRISQKDIEQSIKGETSGSFEDALLAIVKCMRN

||:| ||:|| || | DYRKVLLVLCGGDD 321 07 DYKKALLLLCGEDD 320

80

01-1062

7 GTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLL

Gaps ; 0

Length 321;

; Score 933; DB 14; Length 3; Pred. No. 1e-77; 53; Mismatches 77; Indels

58.3%;

M: Homo sapiens 40-10

184; Conservative

Similarity

F SEQ ID NOS: 363 : FastSEQ for Windows Version 4.0

PLICATION NUMBER: 60/323,580 LING DATE: 2001-09-19

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APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 VYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDP-DAGIDEAQVEQDAQALFQAGELK 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
52.0%; Score 832.5; DB 15;
Best Local Similarity 56.5%; Pred. No. 2.1e-68;
Matches 177; Conservative 48; Mismatches 87;
                                                                                         APPLICANT: Goldon, Gavin

APPLICANT: Goldon, Gavin

APPLICANT: Gullans, Steven R.

APPLICANT: Bueno, Raphael

: TITLE OF INVENTION: Diagnostic and Prognostic Tes

: FILE REFERENCE: B00801/70265 (JRV/JAV)

CURRENT APPLICATION NUMBER: US/10/236,031B

CURRENT FILING DATE: 2002-09-05

PRIOR APPLICATION NUMBER: US 60/317,389

PRIOR FILING DATE: 2002-09-05

PRIOR FILING DATE: 2002-09-05

PRIOR FILING DATE: 2002-08-30

; SOFTWARE: PATENTIN NUMBER: US 60/407,431

; NUMBER OF SEQ ID NOS: 102

; SOFTWARE: PATENTIN Version 3.1
Sequence 18, Application US/10236031B
Publication No. US20030219760A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Application US/10205823 Publication No. US20030108963A1
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Gorbatcheva, Bella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kamatkar, Shubhangi
Wonsey, Angela M.
Glatt, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hoersch, Sebastian
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APPLICANT: Mcnahan, John E.
APPLICANT: Endege, Wilson O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-031B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao, Xumei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-205-823-34
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                           APPLICANT: Rothenberg, Mark E.
TITLE OF INVENTION: No. US20040030110Alel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-322C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 STPEYPAERLPKAMKGLGTRDNTLIRIMVSRSELDMLDIREIFRTKYEKSLYSMIKNDTS 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 245
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NUMBER OF SEQ ID NOS: 470
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57.8%; Pred. No. 1.1e-76;
tive 52; Mismatches 81;
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/114,270 CURRENT FILING DATE: 2002-11-27
                                                                                                                                                                                                                                                                                                                                           PRIOR PAPLICATION NUMBER: 60/281,086
PRIOR PELING DATE: 2001-04-03
PRIOR PELING DATE: 2001-04-03
PRIOR PELING DATE: 2001-04-03
PRIOR PELING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR APPLICATION NUMBER: 60/282,020
PRIOR APPLICATION NUMBER: 60/282,020
PRIOR APPLICATION NUMBER: 60/282,930
PRIOR PILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,930
PRIOR PILING DATE: 2001-04-10
PRIOR PELING DATE: 2001-04-12
PRIOR PELING DATE: 2001-04-13
PRIOR PELING DATE: 2001-04-13
PRIOR PELING DATE: 2001-04-13
         Taupier Jr., Raymond
Casman, Stacie J.
                                                                          Anderson, David W.
Liete, Mario W.
Rastelli, Luca
Edinger, Shlomit R.
                                                                                                                                                                                                       MacDougall, John R.
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Best Local Similarity 57.8
Matches 182; Conservative
                                                                                                                                                                              Stone, David J
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FILE REFERENCE: MRI-044

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126 KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 185
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                                                                                                                                                                                                                                                                                                                                                             KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 245
                                                                                                                                                                                                                                                                                                                                                                                    61 FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
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                                                                                            6 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSRSNAQRQEISAAFKTLFGRDL
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| Patent No. US20020151681A1
| GENERAL INFORMATION:
| APPLICANT: Craig Rosen,
| APPLICANT: Steve Ruben,
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REFERENCE: PAl01
| CURRENT APPLICATION NUMBER: US/09/925,300
| CURRENT FILING DATE: 2001-08-10
| FRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 1890
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 1664
         Length 324;
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                                                 Indels
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48.1%; Pred. No. 2.6e-63;
tive 66; Mismatches 99; Indels
    48.8%; Score 781; DB 14;
48.3%; Pred. No. 1.2e-63;
iive 64; Mismatches 99;
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                                                 Conservative
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US-09-925-300-1664
                           Similarity
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                                                 152;
    Query Match
Best Local S:
Matches 152,
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1 Similarity 50.2%; Pred. No. 2e-66;
158; Conservative 61; Mismatches 96; Indels
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INVENTION: Angiogenesis Modulating Proteins
ERENCE: 8865M
                  FILING DATE: 2002.07.25
LING DATE: 2002.07.25
LING DATE: 2001.07.25
LING DATE: 2001.07.25
LING DATE: 2001.07.25
LING DATE: 2001.08.22
LING DATE: 2001.08.22
PPLICATION NUMBER; 60/314,356
LING DATE: 2001.09.25
PLICATION NUMBER; 60/341,746
LING DATE: 2001.12.12
LING DATE: 2001.12.12
LING DATE: 2001.12.12
LING DATE: 2002.03.05
PPLICATION NUMBER; 60/362,158
LING DATE: 2002.03.05
PR SEQ ID NOS: 455
FRASTSEQ for Windows Version 4.0
APPLICATION NUMBER: US/10/205,823
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T: The Procter & Gamble Company
T: Peters, Kevin
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PLICATION NUMBER: US 60/355,295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262, Application US/10316253 on No. US20030162706A1
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: PatentIn version 3.1
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53-262
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M: Homo sapiens
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US-10-097-340-8
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                                                             APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S65 NKPLYFADRLYDSMKGKGTRDKVLIRIMVSRSEVDMLKIRSEFKRKYGKSLYYYIQQDTK 324
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7 GTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLL 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 339;
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; OTHER INFORMATION: Incyte ID No. US20020156263A1 1378745CD1
US-09-974-298-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                            APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR PILING DATE: 2000-05-10
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL PROGRAM
SEQ ID NO 91
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.3%; Score 708.5; DB 9;
46.3%; Pred. No. 6.2e-57;
tive 63; Mismatches 105;
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US-10-097-340-6
; Sequence 6, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INPERMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel B. MEYERS
; APPLICANT: Rachel B. MEYERS
; APPLICANT: Peter OLANDI
                                                                                                                                                                  Sequence 91, Application US/09974298
Patent No. US20020156263A1
                                                                       468 AGDTSGDYRRLLLAIVGQ 485
                                                     301 KGDTSGDYKKALLLLCGE 318
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Best Local Similarity 46.3%
Matches 146; Conservative
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                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                    RESULT 16
US-09-974-298-91
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TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer PILE REPERBENCE: MRI-030 CURRENT APPLICATION NUMBER: US/10/097,340 CURRENT FILING DATE: 2002-03-14
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/276,025
PRIOR PELING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
PRIOR PELING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR PELING DATE: 2001-09-16
PRIOR PELING DATE: 2001/09/26
PRIOR PILING DATE: 2001/09/26
PRIOR PILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
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Gordon B. MILLS
Robert C. BAST, Jr.
                                                                           Rosemarie SCHMANDT
Xumei ZHAO
Karen GLATT
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Best Local Similarity 46.3%
Matches 146; Conservative
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US-10-097-340-6
                                                         Karen LU
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APPLICATION NUMBER: US/10/097,340 FILING DATE: 2002-03-14

Gordon B. MILLS Robert C. BAST, Jr.

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Karen LU

Peter VEIBY

Ami SEN

Steve G. KOVATS Rachel E. MEYERS Michael MORRISEY Peter OLANDT

Rosemarie SCHMANDT Xumei ZHAO Karen GLATT

PELICATION NUMBER: 60/276, 025
LING DATE: 2001-03-14
LING DATE: 2001-09-26
LING DATE: 2001-09-26
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-881-110
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 110
                                                                                                        Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 615
LENGTH: 327
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                                                                                                                                                                                                                                                                                                                          42.7%; Score 683; DB 9; Length 327; 45.0%; Pred. No. 1.3e-54;
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PTZ07
CURRENT APPLICATION NUMBER: US/09/764,881
CURRENT FILING DATE: 2001-01-17
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45.0%; Pred. No. 2.6e-54;
tive 65; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                   66; Mismatches 100;
                                       FILE REFERENCE: PJZ06
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
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; Sequence 110, Application US/09764881
; Publication No. US20030125246A9
; GENERAL INFORMATION:
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Best Local Similarity 45.03
Matches 136; Conservative
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Best Local Similarity 45.0%
Matches 136; Conservative
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; ORGANISM: Homo sapiens
US-09-764-853-615
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LING DATE: 2001-09-19
PSEQ ID NOS: 363
PSESESEQ for Windows Version 4.0

44.3%;

M: Homo sapiens

RT

40-8

146; Conservative

Similarity

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60/323,580 60/325,102

CLING DATE: 2001-08-10
PPLICATION NUMBER: 60/32
LLING DATE: 2001-09-26
PPLICATION NUMBER: 60/32

615, Application US/09764853 . US20020090672A1 NFORMATION:

53-615

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                                                                                                                      TGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQVYEEEY 133
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CURRENT PILING DATE: 2002-09-13

PRIOR PAPLICATION NUMBER: 09/764,881

PRIOR PILING DATE: 2000-01-31

PRIOR PILING DATE: 2000-01-31

PRIOR PILING DATE: 2000-00-21

PRIOR PLING DATE: 2000-00-20-4

PRIOR PLING DATE: 2000-00-20-4

PRIOR PLING DATE: 2000-06-28

PRIOR PLING DATE: 2000-06-28

PRIOR PLING DATE: 2000-06-28

PRIOR PLING DATE: 2000-06-28

PRIOR PLING DATE: 2000-06-14

PRIOR PLING DATE: 2000-06-14

PRIOR PLING DATE: 2000-07-14

PRIOR PLING DATE: 2000-07-11

PRIOR PLING DATE: 2000-07-14

PRIOR PLING DATE: 2000-07-14
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                      29 GPDVDRDAKKLNKACKGMGTNEAAIIEILSGRTSDERQQIKQKYKATYGKELEEVLKSEL
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GPDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSEL
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ07C1
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Publication No. US20040005577A1
GENERAL INFORMATION:
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NAME/KEY: misc_feature
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US-10-242-747-110
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LENGTH: 332
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DB 15; Length 332

42.5%; Score 680;

Query Match

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APPLICANT: Waisman, David M.
APPLICANT: Waisman, David M.
APPLICANT: Waisman, Mijung
TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
FILE REFERENCE: ME02-001
CURRENT APPLICATION NUMBER: US/10/304,287
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: US 60/333,866
PRIOR FILING DATE: 2001-11-28
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                                                                                                                                             74 TGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQVYEEEY 133
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                                                                                                                                                                                                                                                                          149 DRSLESDVKGDTSGNLKKILVSLLQANRNEGDDVDKDLAGQDAKDLYDAGEGRWGTDELA
                                                                                                                                                                                                                                                                                                                                              29 GFDVDRDAKKLNKACKGMGTNEAAIIEILSGRTSDERQQIKQKYKATYGKELEEVLKSEL
                                                                                                                                                                                                                                                                                                                        FITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRSIPAYLAE
                                                             GFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSEL
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                   Indels
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44.6%; Pred. No. 2.3e-52;
ive 57; Mismatches 98;
45.0%; Pred. No. 2.6e-54;
tive 65; Mismatches 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Sim:larity 44.6%;
Matches 140; Conservative 5
                   Conservative
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SOFTWARE: Microsoft Word
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: manmalian US-10-304-287-2
  Local Similarity
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                        Matches 136;
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301-888

E: PatentIn Ver. |2.0 DF SEQ ID NOS: 1694

888 0 PRT SM: Homo sapiens

301-888

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248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 YEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELKWG 188
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                                                                                                                                                                                                                                                                                           Gaps
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US-09-919-172-39
                                                                                                                                                                                                                                             Best Local Similarity 44.3%; Pred. No. 1e-51;
Matches 137; Conservative 59; Mismatches 113; Indels
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44.0%; Pred. No. 2e-51;
tive 60; Mismatches 113;
                                                                                                                                                                                                                     40.8%; Score 653; DB 12;
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Patent No. US20020119463A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Faris, Mary
APPLICANT: Turner, Christopher M.
ITILE OF INVENTION: PROSTATE CANCER MARKERS;
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR APPLICATION NUMBER: 00/222,469
PRIOR APPLICATION NUMBER: 000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL PROGram
SEQ ID NO 39
LENGTH: 346
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; SEQ ID NO 2250
; LENGTH: 388
; TYPE: PRT
: ORGANISM: Homo sapiens
US-10-276-774-2250
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378 EKILVALCG 386
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 136; Conserval
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TT: Tang, Y, Tom| et al
TY: Tang, Y,
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                                                                                                                                                                                                                        988, Application US/09925301
o. US2002052308A1
INT. ROSO et al.
NT. ROSO et al.
F INVENTION: Nucleic Acids, Proteins and Antibodies FERENCE: PA106
FILING DATE: 2001-08-10
FILING DATE: 2000-03-08
FILING DATE: 2000-03-08
ILING DATE: 2000-03-08
ILING DATE: 1999-03-12
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al Similarity 44.3%; Pred. No. 9.5e-52;
137; Conservative 59; Mismatches 113; Indels
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74-2250 2250, Application US/10276774 on No. US20040053245A1 NFORMATION:

09 KKALLLLCG 317 :| |: ||| 63 EKILVALCG 371 F SEQ ID NOS: 2700

Search completed: March 25, 2004, 08:08:25 Job time : 47 secs

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Sequence 635, Applisequence 635, Applisequence 636, Applisequence 62, Applisequence 62, Applisequence 62, Applisequence 21, Applisequence 21, Applisequence 21, Applisequence 24, Applisequence 24, Applisequence 24, Applisequence 24, Applisequence 24, Applisequence 24, Applisequence 23, Applisequence 23, Applisequence 23, Applisequence 23, Applisequence 26, Applisequence 26, Applisequence 26, Applisequence 26, Applisequence 27, Applisequence 21, Applisequence 
                              Sequence Seq
                                                                                                                                                                                        Sequence Seq
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                   US-09-157-257-6
US-09-157-257-6
US-09-603-186-2
US-09-252-991A-26478
US-09-234-245-4
US-09-234-245-4
US-09-911-927-14
US-09-911-927-14
US-09-911-927-14
US-09-911-927-14
US-09-911-927-14
US-09-911-927-14
US-09-911-927-14
US-09-595-664B-29
US-09-595-664B-29
US-09-723-820-10
US-09-723-820-10
US-09-134-000C-6356
US-09-134-000C-6356
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US-08-823-516-79
US-08-823-516-79
US-08-823-516-136
US-08-759-038-115
US-09-84-938-115
US-09-252-991A-23882
US-09-540-236-3498
US-09-540-236-3498
US-09-540-236-3498
US-09-540-236-3498
US-09-540-252-991A-25928
US-09-90-7252-991A-25928
US-09-90-7252-991A-25928
US-09-398-1868-2
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US-08-630-822A-62
US-09-005-069-62
US-09-171-156A-21
US-09-004-730A-21
US-09-981-799A-21
US-09-107-532A-7128
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US-09-010-1478-24
US-09-724-519-2
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US-09-198-452A-314
US-09-198-452A-1018
US-09-120-365-72
US-09-515-039-72
US-09-613-681A-8049
US-09-543-681A-8147
US-09-328-352-6501
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US-08-418-893D-24
US-09-914-259-11
US-09-914-259-56
US-07-730-953-2
US-07-730-953-2
US-09-328-352-5426
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US-09-308-375-2
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Sequence 1, Appli
Patent No. 5225537
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Sequence 2
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/cgn2 6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2 6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2 6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2 6/ptodata/2/jaa/PCTUS COMB.pep:*
/cgn2 6/ptodata/2/jaa/PCTUS COMB.pep:*
                   Copyright (c) 1993 - 2004 Compugen Ltd
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US-08-948-276-1
5225537-4
US-09-324-096A-4
US-09-324-096A-6
US-09-324-096A-6
US-08-948-276-3
US-08-948-276-3
US-08-948-276-3
US-08-948-276-3
US-08-948-276-3
US-08-526-136-14
US-09-521-172-39
US-09-912-976-490
US-09-325-932A-65
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5-09-325-932A-63
5-09-325-932A-64
5-08-923-511-2
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Maximum Match 100%
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1 MAQVLRGTVTDFPGFDERAD
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seq length: 200000000
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653 649 1.5 8.5 261 232 128

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; TYPE: PRT
; ORGANISM: human
US-08-948-276-1
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                                                                                                                                                                                                                                                                 TE: OBLON, SPIVAK, McCLELLAND; MAIER & NEUSTADT, RE: P.C. 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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100.0%; Pred. No. 6.4e-144;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHWINGRE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,746
FILING DATE: 24-SEP-1993
                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: SATIO, YUSHI
APPLICANT: SATIO, ANIO
APPLICANT: SUDA, MAKOTO
TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Oblon, No. 5591633man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-074-0 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEPHONE: (703)
                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/807,623
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 037227/1987
FILING DATE: 20-FEB-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 184428/1987
FILING DATE: 23-JUL-1987
ATTORNEY/AGENT INPORMATION:
NAME: Oblon, No. 5591633man F.
                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                  Sequence 3, Application US/08125746
Patent No. 5591633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
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amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                  CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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ADDRESSEE:
STREET: 175
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                       241 VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
                                                                                                          241 VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
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; Pred. No. 6.4e-144;
0; Mismatches . 0;
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PAPLICANT: FOSTER, DONALD

TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID
PHOSPHOLIPID-BINDING PROTEINS
NUMBER OF SEQUENCES: 14

CURRENT APPLICATION DATA:
PELLING DATE: 29-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ernst, Joel D.
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UCSF97-113
CURRENT APPLICALION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGD/TSGDYKKALLLLCGEDD 320
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Patent No. 6511829
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ilarity 100.0%;
Conservative 0
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; LENGTH: 320
5225537-4
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APPLICANT: Brown, David
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
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1.9e-143;
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Pred. No. 5.9e-143;
0; Mismatches 1;
                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: US/09/324,096A NUMBER OF SEQ ID NOS: 12 SOFTWARE: Patentin version 3.0 I DNO 2
                                                                                                                                                                                       Score 1595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09324096A
Patent No. 6323313
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100.0%;
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99.7%;
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Best Local Similarity 99.7
Matches 319; Conservative
248855 OPAT UR
                                                                                                                                                                                                                                 Conservative
                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                            : 319 amino aci
amino acid
                                                                                                                       , MOLECULE TYPE: protein US-08-125-746-1
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ORGANISM: Homo sapiens
                                                                                                          unknown
                                                                                                                                                                                                       Best Local Similarity
Matches 319; Conserv
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                                                                                                     TOPOLOGY:
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                                                            LENGTH:
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                                                                                                                                                                                       61 FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
                                                                                                                                                                                                                                                                            21 ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF 180
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                     Length 320;
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                                                                Indels
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                                           6.4e-144;
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                     Score 1600; DB 6;
Pred. No. 6.4e-144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF INVENTION: ANTICOAGULANT POLYPEPTIDE OF SEQUENCES: 5
                                                                0; Mismatches
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NG DATE: 20-FEB-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UM TYPE: Floppy|disk
UTER: IBM PC compatible
ATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01 KGDTSGDYKKALLLLLCGEDD 320
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                       100.0%;
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ICATION NUMBER: US 07/
NG DATE: 13-DEC 1991
APPLICATION DATA:
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EY/AGENT INFORMATION:
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                                                                Conservative
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ANT: IWASAKI, AKI
ANT: SUDA, MAKOTO
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UM TYPE: Floppy
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VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 300
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                                                                                                                                                Score 1590; DB 4;
Pred. No. 5.9e-143;
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Pred. No. 2.5e-133;
9; Mismatches 9;
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TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UCSP97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                      0; Mismatches
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; Sequence 2, Application US/08948276
Patent No. 6511829
; GENERAL INFORMATION:
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                                                                                                                                                99.4%;
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Best Local Similarity 94.0
Matches 297; Conservative
    version
                                                                                                                                                                                        Conservative
                                                                                     sapiens
                                                                                                                                                                   Similarity
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US-08-948-276-2
                                                             TYPE: PRT
ORGANISM: Homo
SOFTWARE: Pate
SEQ ID NO 6
LENGTH: 327
                                                                                                      US-09-324-096A-6
                                                                                                                                                                                      Matches 319;
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                                            QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV 247
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    QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
                                                                                     VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
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                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09324096A
Patent No. 6323313
Regrent No. 6323313
APPLICANT: Tait, Jonathan
APPLICANT: Brown, David
APPLICANT: Tait, Jonathan
APPLICANT: True OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
FILE REFERENCE: UOFW-1-13841
CURRENT APPLICATION NUMBER: US/09/324,096A
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.0
SEQ ID NOS: 12
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Patent No. 6323313
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tait, Jonathan
APPLICANT: Brown, David
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
FILE REPERENCE: UOFW-1-13841
CURRENT APPLICATION NUMBER: US/09/324,096A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 12
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Pred. No. 5.9e-143;
0; Mismatches 1;
                                                                                                                                                                     KGDTSGDYKKALLLLCGEDD 320
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99.7%;
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Best Local Similarity 99.7
Matches 319; Conservative
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; ORGANISM: Homo sapiens
US-09-324-096A-4
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US-09-324-096A-4
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US-09-324-096A-6
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245

125 123 185

65 63

Gaps

1;

240 247 307

180 187

120

9 67

Gaps

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GDYKKALLLLC-GEDD 320

246 244 906 276-3

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65 LLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 LRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 RSIPAYLAETLYYAMKGAGTDDHTLIRVIVSRSEIDLFNIRKEFRKNFATSLYSMIKGDT
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COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM
COMPUTER: STEM: PC-DOZID16
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,975A
FILING DATE: 11-NOV-1993
CLASSIFICATION: 436
ATTORNEY AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 04843/016001
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
TELEPKX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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Patent No. 6511829
GENERAL INFORMATION
TITLE OF INVENTION GFP-Annexin Fusion Proteins
FILE REFERENCE: USSF97-113
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SEQ ID NOS: 6
SEQ ID NOS: 6
SEQ ID NO 4
LENGTH: 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.1%; Score 1457.5; DB 2
91.8%; Pred. No. 2.2e-130;
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                                                                                                                                                                                                                                                                                                                                                       TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 291; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-149-975A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-948-276-4
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                         SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 305
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2 LRGTVTDFSGFDGRADAEVLRKAMKGLGTDEDSILNLLTARSNAQRQQIAEEFKTLFGRD 61 5 LRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRD

Gaps 1;

DB 4; Length 318; 12; Indels

; Score 1464.5; DB ; ; Pred. No. 4.7e-131; 12; Mismatches 12;

ch al Similarity 92.18 292; Conservative

3M: rat 276-3 318

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3, Application US/08948276
5. 6511829
INPOMATION:
FINUMATION:
FINUMETRICATION WIMBER: US/08/948,276
FILING DATE: 1997-10-09
FEED NOS: 6

3: PatentIn Ver.

82 LKWGTDEEKFITILGTRSVSHLRRVFDKYMTISGFQIEETIDRETSGNLENLLLAVVKSI

OF INVENTION: DIAGNOSTIC ASSAYS FOR ALZHEIMER'S OF INVENTION: DISEASE OF SEQUENCES: 5 PONDENCE ADDRESS:

2, Application US/08149975A . 5849600

75A-2

ANT: Nixon, Ralph ANT: Honda, Toshiyuki

INFORMATION:

05 SGDYKKALLLLC-GEDD 320 SGDYKKALLLCGGEDD 318

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85

ESSEE: Fish & Richardson P.C. ET: 225 Franklin Street

Boston USA

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N/A

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TELEX: 200154
INFORMATION FOR SEQ ID NO:
STRANDEDNESS:
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TOPOLOGY:
US-08-526-136-14
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                                                                                                                                                                                                                                                                                                                                     247 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG 306
                                                                                                                                                                                                                                                                                                                                                       67 DDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 126
                                                                                                                                                             7 GTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLL
                                                 Gaps
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                   Length 321;
                                                 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
COMPUTER: IBM PS/2 Model 50Z or 55SX
COMPUTER: WordPerfect (Version 5.0)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
                 58.3%; Score 933; DB 4;
llarity 58.6%; Pred. No. 1.5e-80;
Conservative 53; Mismatches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 et al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08526136; Patent No. 6107089; GENERAL INFORMATION: APPLICANT: Towle, Christine A. et TITLE OF INVENTION: ANNEXIN XI NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
- APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY, AGENT INFRWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fish & Richardson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                    Similarity
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                                                 184;
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                    Query Match
                                        Best Local
Matches 18
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245
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                                                                                                                                                                                            QVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELK 186
                                                                                                                                                                                                                                                                                                    185
                                                                                                                                                                                                                                                                                                                                           WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS 246
                                                                                                                                                                                                                                                                                                                                                                                                                             247 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 KSAYFAERLYKSMKGLGTDDDTLIRVMVSRAEIDMLDIRANFKRLYGKSLYSFIKGDTSG 305
                                                                                                                                                                                                                                                                                7 GTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLL
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0
57.8%; Score 924; DB 3; Length 319; 58.3%; Pred. No. 1e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 021:0-2804
COMPUTER RENDABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPIJICATION DATA:
APPLICATION NUMBER: US/08/526,136
FILING DATE:
                                             51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGBNT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Towle, Christine A. et al
TITLE OF INVENTION: ANNEXIN XI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08526136
Patent No. 6107089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30,162
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REGISTRATION NUMBER: 30,1
REFERENCE/DOCKET NUMBER:
                            58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYFIXALLLLCGEDD 320
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      Query Match
Best Local Similarity 58.3%
Matches 183; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 435
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KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 245
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                                                                                                                                                                                                                                                                     126 KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 185
                                                                                                                                                                                                                                                                                                                                                                                                                 146 SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                                               Gaps
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                                                                                                         DB 3; Length 503;
                                                                                                                                           83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UTER: IBM PS/2 Model 50Z or 55SX
THIG SYSTEM: IBM P.C. DOS (Version 3.30)
WARE: WordPerfect (Version 5.0)
T APPLICATION DAȚA:
                                                                                                       tch 54.7%; Score 875; DB 3; al Similarity 55.2%; Pred. No. 9e-75; 174; Conservative 58; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : Clark, Paul T.|
STRATION NUMBER: | 30,162
RENCE/DOCKET NUMBER: 00786/099001
MMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02110-2804
ER READABLE FORM:
UM TYPE: 3.5" Diskette, 1.44 Mb
UTER: IBM PS/2 Model 50Z or 55SX
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APPLICATION DATA:
ICATION NUMBER: US/08/214,036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ICATION NUMBER: |US/08/526,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ICATION NUMBER: 07/837,775
NG DATE: February 13, 1992
ICATION NUMBER: 07/764,465
NG DATE: September 23, 1991
EX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4, Application US/08526136
6107089
INFORMATION:
OF INVENTION: ANNEXIN XI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PONDENČE ADDRESS:
ESSEE: Fish & Richardson
ET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||:| || :|| :|
GDYRKILLKICGGND 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06 GDYKKALLLLCGEDD 320
NCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Boston
E: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF SEQUENCES:
                                    E: amino acid
DLOGY: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRY: U.S.A.
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                                                                                                                                                                                                             189
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250
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                                                                                                                                                                                                                                                                                                       251 IKDLKSELSGNFEKTILALMKTPVLFDAYEIKEAIKGAGTDEACLIEILASRSNEHIREL 310
                                                                                                                                                                                                                                                                                                                                                      126 KQVYEEBYGSSLEDDVVGDŢSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 185
                                                                                                                                                                                                                                                                                                                                                                          186 KWGTDEBKFITIFGTRSVSHLRKVFDKYMTISGPQIEETIDRETSGNLEQLLLAVVKSIR 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KWGTDEEKPITIFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
                                                                                                                                                                                                                                           191 KGTITDASGFDPLRDAEVLRKAMKGFGTDEQAIIDCLGSRSNKQRQQILLSFKTAYGKDL
                                                                                                                                                                                                            6 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI
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                                                                                                                                                                                 .
                                                                                                                                               Length 505;
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                                                                                                                                                                            83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08948276
Patent No. 6511829
Fatent No. 6511829
FAPLICANT: Ernet, Joel D.
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REPRENCE: UCSP97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 323
                                                                                                                                           Score 875; DB 3;
Pred. No. 9.1e-75;
                                                                                                                                                                          58; Mismatches
                                                                                                                                         54.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 GDYKKALLLLCGEDD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||:| || :| :|
491 GDYRKILLKICGGND 505
                                                                                                                                                          Best Local Similarity 55.2
Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.2%
Matches 158; Conservative
                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                    TYPE: amino acid
TOPOLOGY: N/A
 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: human
US-08-948-276-5
                                                                                                     US-08-526-136-4
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TELEX:
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                                                                   TYPE:
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Matches 137; Conservative
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Best Local Similarity
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ORGANISM: human
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189 RWGTDEDKFTEILCLRSFPQLKLTFDEYRNISQKDIVDSIKGELSGHFEDLLLAIVNCVR 248
                                                                                                   249 NTPAFLAERLHRALKGIGTDEFTLNRIWVSRSEIDLLDIRTEFKKHYGYSLYSAIKSDTS 308
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                                                                   SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
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48.1%; Pred. No. 8.5e-66;
tive 66; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTATION OF STATE 
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: TOWIE, Christine A. et TITLE OF INVENTION: ANNEXIN XI NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS: ADDRESSER: Fish & Richardson STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/08526136
Patent No. 6107089
GENERAL INFORMATION:
                                                                                                                                                                                                       GDYKKALLLLCGEDD 320
                                                                                                                                                                                                                                                                 309 GDYEITLLKICGGDD 323
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: N/A
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Best Local Similarity
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STATE: Massachus
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-526-136-13
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                                                                 9 VTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDD
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44.3%; Pred. No. 6.4e-54;
Live 59; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: GFP-Annexin Fusion Proteins;
FILE REFERENCE: UCSF9-113;
CURRENT APPLICATION NUMBER: US/08/948,276;
CURRENT APPLICATION NUMBER: US/08/948,276;
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: FAIS, MARY
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 39, Application US/09919172
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Patent No. 6511829
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449_AGDTSGDYRRLLLAIVGQ 466
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346 33 RT

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GENERAL INFORMATION:

APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant develo
TITLE OF INVENTION: death and their use in the modification of forestry plant develo
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 QKTGEHKTMLQMILCNKSYQQLRLVPQEFQNISGQDWVDAINECYDGYFQELLVAIVLCV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 IKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 LKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 RSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 RDKPAYPAYRLYSAIHDFGFHNKTVIRILIARSEIDLLTIRKRYKERYGKSLFHDIRNFA 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 DCEQLRTAFAGWGTNEKLIISILGHRNAAQRKLIRQTYAETYGEDLLKALDRELTNDFER
                                                                                                                                                                                                                                                                                                                                                                1; Gaps
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                                                                                                                                                                                                                                                                                                                37.0%; Score 591.5; DB 4;
38.1%; Pred. No. 4e-48;
tive 76; Mismatches 118;
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23.7%; Score 378.5; DB 4;
Best Local Similarity 32.1%; Pred. No. 6.6e-28;
Matches 96; Conservative 58; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
    REGISTRATION NUMBER: 41,119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 62, Application US/09325932A
Patent No. 6451604
                             REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
                                                                                                                                                        LENGTH: 324 amino acids
                                                                    TELEPHONE: 301-309-8504
                                                                                    TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGDYKKALLLLCGED 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 SGHYKKALLAICAGD 320
                                                                                                                                                                                                                                                                                                                                                       Matches 120; Conservative
                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Pinus radiata
US-09-325-932A-62
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                     US-09-010-147B-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 LKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 YEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELKWG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 TDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRSIP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 AYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSGDY 308
                                                                                                                                                                                                                                                                                                                                                         9 VTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDD 68
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44.0%; Pred. No. 1.5e-53;
Live 60; Mismatches 113; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
RRENT APPLICATION DAIR:
                                                                                                                                                                        :Y: misc_feature |
:NFORMATION: Incyte ID No. 6673545 1303785CD]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 12-No. 6653445-2002
CLASSIFTCATION: «Unknown»
IOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
APPLICATION NUMBER: US 60/034,204
FILING DATE: 21-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/010,147B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLICANT: Ni et al.
TLE OF INVENTION: Human Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/09010147B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20850 | MPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jonathan L. Klein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TORNEY/AGENT INFORMATION
ILING DATE: 2000-07-28
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                                                                                                                                                                                                                                                                                     11 Similarity 44.0%
136; Conservative
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36 EKILVALCG 344
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. 6653445
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COUNTRY: USA
                                                                                                                               M: Homo sapiens
                  JF SEQ ID NOS: 1
3: PERL Program
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INFORMATION:

47B-16

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APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant develor
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: PastSEQ for Windows Version 3.0
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Beguence 4, Application US/09157257

Betent No. 6375954

GENERAL INFORMATION:
APPLICANT: DUTTA, Sukanta K.
APPLICANT: BISWAS, Biswajit
APPLICANT: BISWAS, Biswajit
APPLICANT: BISWAS, Biswajit
APPLICANT: BISWAS, BISWAJIC Ramesh
TITLE OF INVENTION: A SIZE-VARIABLE STRAIN-SPECIFIC PROTECTIVE ANTIGEN FOR TITLE OF INVENTION: POTOMAC HORSE FEVER
FILE REPERENCE: 8172-9016
CURRENT APPLICATION NUMBER: US/09/157,257
CURRENT FILING DATE: 1998-09-18
BARLIER APPLICATION NUMBER: 60/059,252
BARLIER PILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                  SVILWTLDPAERDAFLSNEATKRLTSSNWVLMEIACTRSSMELFMVRQAYHARYKKSLEE 135
                                                                                                                                                                                                                                              140 DVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELKWGTDEEKFITIFG 199
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                                                                                         16 DAEQLQKAFAGWGTNEDLIISILPHRNAAQRKVIRQTYAETYGEDLLKALDKELSSDFER
                                                                                                                                                       80 LIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQVYEEEYGSSLED
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                      1; Gaps
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                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.5%; Score 232; DB 4; L
35.0%; Pred. No. 2.5e-14;
tive 33; Mismatches 73;
ilarity 28.9%; Pred. No. 1.9e-15;
Conservative 46; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-325-932A-66
; Sequence 66, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
    Similarity
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    Local
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APPLICANT: Flinn, Barry
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant develo
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 EQLLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 LVVLWSLDPAERDAYLANEATKRWTSSNQVLMEIACTRSPQQLLMARQAYHARYKKSMEE 135
                                                DVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQ-AGELKWGTDEEKFITIF 198
                                                                                                                                         199 GTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRSIPAYLAETLYYA 258
                                                                                                                                                                  DVAHHTTGDFRKLLVPLGSSYRNDGDEVNMTLAKAEAKILHEKISEKAYG--HEDLIRIL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 QDAMYLWEACQQKTGEHKTMLQMILCNKSYQQLRLVFQEFQNISGQDWVDAINECYDGYF 63
                                                                                                                                                                                                                                MKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSGDYKKALLLLCG 317
                                                                                                                                                                                                                                                         Gaps
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16.3%; Score 261; DB 4;
Best Local Similarity 38.4%; Pred. No. 3.3e-17;
Matches 56; Conservative 29; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human
FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: PATENT, pm
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Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 65, Application US/09325932A
Patent No. 6451604
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US-09-325-932A-65
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CORGANISM: Homo sapiens
US-09-621-976-4980
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US-09-325-932A-65
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LENGTH: 239
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DB 4;

15.3%; Score 245.5;

Query Match

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: Flinn, Barry |
F: Lasham, Annette
INVENTION: Compositions affecting programmed cell
INVENTION: death and their use in the modification of forestry plant develc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 KYMTISGFQIEETIDRETSGNLEQLLLAVVK-SIRSIPAYLAETLYYAMKGAGTDDHTLI 270
                                                                                                                                                                                                                                                      78 EKLIVALMKPSRLYDAY----ELKHALKGAGTNE--KULTE------IIASRTPE 120
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1 Similarity 32.9%; Pred. No. 0.00051,
27; Conservative 19; Mismatches 36: Тидл1
                                                                                                                                        ch 8'.0%; Score 128; DB 4; Length 849; I Similarity 23.3%; Pred. No. 0.0017; 81; Conservative 62; Mismatches 132; Indels
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PatentIn Ver. 2
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Q804g3 brachydanio Q90x16 xenopus lae Q921f1 mus musculu Q804g7 brachydanio	Q8k2n9 mus musculu Q95154 bos taurus	Q8C1x9 mus musculu Q8C1x9 mus musculu Q8vin2 rattus norv	Q8bp75 mus musculu Q8igj8 drosophila	Q9n161 bombyx mori	Q9ng55 drosophila Q8wpg9 bombyx mori	Q8wph0 bombyx mori Q9gng6 bombyx mori	Q2MITEU DOMDYX MOII : Q27512 caenorhabdi O8tbv2 homo sapien	07sz98 xenopus lae 0969d3 drosophila	Q9czı/ mus musculu Q7zxm2 xenopus lae Q95v57 artemia san	099jg3 mus musculu Q7t3a8 brachydanio	Q804h2 brachydanio Q8mjb5 oryctolagus	O93446 Oryzias lac Q86dv3 schistosoma O804h0 brachydanio	Q7szll xenopus lae	Q9vxg3 drosophila Q9vxg3 drosophila	O98sh7 brachydanio	Q804g9 brachydanio	Q804g8 brachydanio	Q804gz brachydanio Q27864 caenorhabdi	Q8ccv9 mus musculu Q8bsl2 mus musculu	Q7zwx0 xenopus lae Q27473 caenorhabdi	Q99kh3 mus musculu	057570 brachydanio	O9xz19 taenia soli	Q9c9x3 arabidopsis Q9bi01 globodera p	Q9d272 mus musculu O9nqu7 taenia soli	09c5v4 arabidopsis	Q84q48 oryza sativ	Q9r0v2 mus musculu Q9zr53 medicago sa	Q8itj0 heterodera	O9fug5 ceratopteri	Q9xens nicotiana t Q9fug6 ceratopteri	O65848 medicago tr	P93158 gossypium n O59907 neurospora
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
-!- SIMILARITY: ONTAINS 4 ANNEXIN FAMILY.
-!- SIMILARITY: ONTAINS 4 ANNEXIN REPEATS.
--- SIMILARITY: AAH18611; -- GO GO: 0005509; F: calcium ion binding; IEA.
GO; GO: 0005544; F: calcium-dependent phospholipid binding; IEA.
                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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Last annotation update)
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Pred. No. 4.8e-107;
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Pfam; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
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Best Local Similarity 99.7'
Matches 319; Conservative
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                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
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01-MAR-2002 (
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Submitted (FBS-201) to the EMBL/GenBank/DDBJ databases.

L. Submitted (FBS-201) to the EMBL/GenBank/DDBJ databases.

CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).

CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).

C. I. SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

C. I. SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.

REMBL; BC003716; AAH03716.1; ...

RMD; MG1.16608; AAR8.

RGJ; GC:0005569; F:calcium ion binding; IEA.

GO; GC:0005509; F:calcium-dependent phospholipid binding; IEA.

RGJ; GC:0005509; F:calcium-dependent phospholipid binding; IEA.

REMBL; PRO0196; ANNEXIN,

RRINTS; PR00196; ANNEXIN;

RRINTS; PR00196; ANNEXIN;

RRINTS; RRINTS; RRO0196; ANNEXIN;

RRINTS; RRINTS; RRINTS; RRO0196; ANNEXIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.8%; Score 1484.5; DB 11; Length 319; 93.7%; Pred. No. 4.5e-99; ive 9; Mismatches 10; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 319 AA; 35738 MW; 52E2C7CCEA386917 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                            KGDTSGDYKKALLLLCGEDD
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                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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306 GDYKKALLLLCGEDD 320
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                                                                                                                                                                                                                                                         Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.
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Best Local Similarity 75.6
Matches 238; Conservative
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     Xenopodinae; Xenopus
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                                                                            FROM N.A
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                          NCBI_TaxID=8355;
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                                                                                 SEOUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 RSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
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                                                                                                                                                                             ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                     ota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
ia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00335; ANX; 4!
E; PS00223; ANNEXIN; 3.
n; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 86.9%; Score 1390; DB 11; Length 302; 1 Similarity 92.0%; Pred. No. 2.7e-92; 276; Conservative 12; Mismatches 12; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 302|
302 AA; 33965 MW; AB9FB40934A3D007 CRC64;
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-2003 (TrEMBLrel: 25, Last sequence update)
-2003 (TrEMBLrel: 25, Last annotation update)
etical protein (Fragment)
                                               : 1998 (TrEMBLrel: 07, Created)
-1998 (TrEMBLrel: 07, Last sequence update)
-2003 (TrEMBLrel: 25, Last annotation update)
  Ā
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  302
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PRELIMINARY;
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                                                                                                                                                     norvegicus (Rat)
                                                                                                                        ortin V (Fragment
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Antschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Antschul R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan R.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Bukzyainski M.I., Skalska U., Sachilus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-length human and many and many of the state of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
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"Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein S., Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
EMBL; BC054175; AAHS4175.1; -.
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182 245 242 305

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NCBI_TaxID=7955;
                NCBI_TaxID=8090;
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SEQUENCE
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                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 KWGTDEEKFITILGTRSISHLRKVFDKYMTISGYQIEESIDRETSGHLENLLLAIVKSVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 SIPEYLADTLYHAIKGAGTDDCTLIRVMVSRSEIDLLDIKEKFRKNFGKSLHAMIQGDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
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Retraprotas Metazoa; Chordata, Craniata; Vertebratas Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.(Fragment).
Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
                                                                                                                                                                                                                             Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                      Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 AA; 39321 MW; FF71B665A38CA8AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.4%; Score 1255; DB 13; 75.6%; Pred. No. 1.8e-82; ive 44; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 AA
                                                              351
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01-NOV-1998 (TrEMBLrel. 08, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D000143; Annexin; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 GDYRNALLICGGDD 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001464; Annexin
                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC043882; AAH43882.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000143; Annexin;
SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN;
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Matches 238; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00196; ANNEXIN.
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                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00191; annexin;
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                                                                                                                                                                                                                                           Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   IISSUE=Embryo;
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SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFAISLYSMIKGDIS 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 KOVYEEEYGSSLEDDVVGDTSGYYQRMLVVILLQANRDPDAGIDEAQVEQDAQALFQAGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                    FORM ONE BINDING SITE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
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                                                                                                                                                                                                                                                                                                                                                                 EMBL, Y11253, CAA72123.1, -.
HSSP, P17153, 1ALA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 1052; DB 13; Length 317; Pred. No. 7e-68; 48; Mismatches 61; Indels 2
                                                                                                      MEDLINE=99025617; PubMed=9809745;
Osterloh D., Wittbrodt J., Gerke V.;
Characterization and developmentally regulated expression annoxins in the killifish medaka.";
DNA Cell Biol. 17:835-847(1998).
-!- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34765 MW; AFD618681BAFF0FE CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                           CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ANNEXIN PAMILY.
-!- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 AA
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64.8%;
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ProDom; PD000143; Annexin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00191; annexin; 4.
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Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00335; ANX; 4
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185

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65 63

BC046873; AAH46873.1;

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RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
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(TrEMBLrel. 23, L
(TrEMBLrel. 25, L
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ProDom; PD000143; Annexin; 6.
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PROSITE; PS00223; ANNEXIN; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 GDYKKALLLLCGEDD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 GDYRKTLLLCGGDD 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00191; annexin; 6.
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01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 VNDLKSELGGKFEDLIVALMTPPIIYEVTCLRNAIKGAGTDEKVLIEILASRSPNEVNEI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 KSSYKREHDKDLEEDVTGDTGGHFERMLAVLLQASR--QQGIQESLIQSDAQALFAAGEQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 305
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ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
pterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
idae; Danio.
                                                                                                                                                                                                                                                                                                                                                                             2;
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0:0005509; Ficalcium ion binding; IEA.
0:0005549; Ficalcium dependent phospholipid binding; IEA.
0:0005544; Ficalcium dependent phospholipid binding; IEA.
0:0001941; Annexin.
0:0001941; Annexin.
0:000195; ANNEXIN.
0:00035; ANNEXIN; 4.
0:00035; ANNEXIN; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.2%; Score 1027; DB 13; Length 317; 64.4%; Pred. No. 4.5e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.1%; Score 1025; DB 13; Length 317; 64.4%; Pred. No. 6.2e-66; tive 49; Mismatches 61; Indels 2.
                                                                                                                                                                                                                                                                                                                                                                             49; Mismatches 61; Indels
                                                                                                                                                                                                                                 netical protein. |
ICE 317 AA, 35060 MW; B33DA22F3DFBBED5 CRC64;
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; PD000143; Annexin; 4.
SM00335; ANX; 4!
E; PS00223; ANNEXIN; 4.
CC 317 AA; 35057 MW; 082CF83C9F29D6AF CRC64;
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-2003 (TrEMBLrel! 25, Last annotation update)
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ebrafish Annexin|Gene Family.";
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02 GDYRKTLLLCGGDD 316
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PF00191; annexin; 4.
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203; Conservative
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1 Similarity 64.49
203; Conservative
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                                                                                    66 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
                                                                                                                                                                                                                                                                                                                                 186 KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 SVPGYFADSLYAAMKGAGTDDQTLIRIMVTRSEVDLLDIRAEPRKRFATSLHKMIQSDTS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEDLKYELTGKFERLIVNLMRPLAYCDAKEIKDAISGVGTDEKCLIEILASRTNEOMHQL 130
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4 RGTVKPQSGFNANSDAEVLYKAMKGLGTDEDSILQLLIKRSNGQRPEIKAAYKTLHGKDL
                                                                                                                       6 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
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the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
(60,770 full-length cDNAs.";
Nature 420:563-573(2002).
BMBL; AR010342; BAC25291.1;
BMBL; AR010342; BAC25291.1;
GO; GO:0005599; F:calcium ion binding; IEA.

GO; GO:0005594; F:calcium dependent phospholipid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       476 AA; 53669 MW; 9390C5B5E6653D24 CRC64;
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Last annotation update)
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SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
BMBL; AK030728; BAC27101.1; -.
BMBL; AK030728; F.calcium ion binding; IEA.
GO; GO:0005509; F.calcium dependent phospholipid binding; IEA.
                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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; Pred. No. 2.5e-59;
48; Mismatches 80;
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                                                                                                                                                                                       673
                                                                                                                                                                                                                          Created)
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              673 AA; 75885 MW;
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ProDom; PD000143; Annexin; 8.
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                                                                                     GEYKKALLKLCGGDD 325
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                                                           GDYKKALLLLCGEDD
                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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SEQUENCE FROM N.A.
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                                                                                                                                                    RESULT 11
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       70
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                                                                                                                                     SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Strausberg R.; Strausberg R.; Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- DOWAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE ICALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
-!- SIMILARITY: CONTAINS TO THE ANNEXIN FAMILY.
-!- SIMILARITY: CONTAINS 8 ANNEXIN REPEATS.
EMBL; BC005595; AAH05595.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00335; ANX; 8.
PROSITE; PS00223; ANNEXIN; 8.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:88255; Anxa6.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
InterPro; IFR001464; Annexin.
Pro19 Pro19; Annexin.
PRO19; PRO019; Annexin.
PRODOM; PRO01943; Annexin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 58.9%; Score 942; DB 11; Best Local Similarity 59.4%; Pred. No. 1.8e-59; Matches 187; Conservative 49; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                           667 AA
                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 17, CTrEMBLrel. 17, I
                                                                                                                                                                                                               GDYKKALLLCGEDD 320
                                                                                                                                                                                                                                     |:|||||| ||| ||
311 GEYKKALLKLCGGDD 325
                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similar to annexin A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001
01-OCT-2003
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Last sequence update) Last annotation update)

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319 AA

PRELIMINARY (TrEMBLrel! (-2003 (TrEMBLrel) sculus (Mouse).

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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A post both of the collins of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 NOVPKAENKKSLEDAISGDTSGHFRRLLVSLAQGNRDESENVDISIAKTDAQALYQAGEN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KWGIDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI
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                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
EMBL; BC053208; AAH53208.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483 AA; 51425 MW; E4F7F527E30F6DD7 CRC64;
                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.2%; Score 915; DB 13;
57.5%; Pred. No. 9.8e-58;
tive 53; Mismatches 81;
   483 AA.
                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Danio rerio)
                                                          Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932
                                              "...ocr-2003 (TrEMBLrel. 25, La
..-ocr-2003 (TrEMBLrel. 25, La
Hypothetical protein.
Brachydanio rerio
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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-=FVB/N; TISSUB-Breast tumor;

IB=2138825; PubMed=1247932;

IB=2238825; PubMed=12479;

IB S. PubMed=12479;

ID S. PubMed=12479;

ID S. Reberg B. B., Buetow K.H., Schaefer C.F., Bhat N.R.,

IN S. P., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

IN S. P., Collins F.S., Wagner L., Schaefer C.F., Bhat N.R.,

IN S. P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

IS R. P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

IS R. P., Jordan H., Bonaldo M.F., Caravant T.L., Scheetz T.E.,

IS R. P., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

G.S. Worley R.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

John M. Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Jeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Juez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Marra M. M., A., Shallska U., Smailus D.E., Schnerch A., Schein J.E.,

J. Marra M. A., Schein J.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG 306
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11; Length 319;

57.6%; Score 925; DB 11; Length 3.

181; Conservative

67 99 27 26

Similarity

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06 DYRKVLLILCGGDD 319 DYKKALLLLCGEDD 320

07

berg R.; ted (AUG-2003) to the EMBL/GenBank/DDBJ databases. BC055871; AAH55871.1; -. ICE 319 AA; 35929 MW; D962B63D7933F929 CRC64;

Natl. Acad. Sci., U.S.A. 99:16899-16903 (2002).

use cDNA sequences.

ICE FROM N.A.
|=FVB/N; TISSUE=Breast tumor;

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NCBI_TaxID=8090;
NCBI_TaxID=8090;
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         [1]
SEQUENCE
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                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 NOVFKAENKKSLEDAISGDTSGHFRRLLVSLAQGNRDESENVDISIAKTDAQALYQAGEN 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 305
                                                                                                                                                                                                                                                                                                                                                                                       6 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                            Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii, Teleostei; Buteleostei; Neoteleostei;
Acauthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
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0
                                                                                                                                                                                          EMBL; AY178801; AAO20275.1; -.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
                                                                                                                                                                                                                                                                                                                                   526;
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                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                              526 AA; 55732 MW; B54010208D8F79F1 CRC64;
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Last annotation update)
                                                               Last annotation update)
                                                                                                                                                                                                                                                                                                                                                       81,
                                                     Last sequence update)
                                                                                                                                                                                                                                                                                                                                 57.2%; Score 915; DB 13;
llarity 57.5%; Pred. No. 1.1e-57;
Conservative 53; Mismatches 81;
                                                                                    Brachydanio rerio (Zebrafish) (Danio rerio).
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                      Z
                                                                                                                                                 SEQUENCE FROM N.A.
Farber S.A., Olson E.S., Halpern M.E.
"The Zebrafish Annexin Gene Family.";
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InterPro; IPR006031; XYPPX.
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08,
25,
                                         (TrEMBLrel. 24, (TrEMBLrel. 24,
                                                     01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
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ProDom; PD000143; Annexin;
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PROSITE; PS00223; ANNEXIN;
                                                                                                                                                                                                                                              Pfam; PF00191; annexin; 4. Pfam; PF02162; XYPPX; 8.
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01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                  Genome Res. 0:0-0(2003).
                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 181; Conserv
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                                                                          Annexin 11a.
                                          -JUN-2003
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SEQUENCE .
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                                Q804G4;
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                      Q804G4
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Matches
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 LDDILKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KWCTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostcmi;

Actinopterygii; Neopterygii; Neopterygii; Neopterygii; Percomorpha; Actanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Beloniformes; Adrianichthyldae; Oryzinae; Oryzias.
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Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.8%; Score 876; DB 13; Length 320; 54.8%; Pred. No. 3.5e-55; ive 59; Mismatches 82; Indels
             OSTETION D., Withbrook J., Gerke V.;
"Characterization and developmentally regulated expression amexins in the killifish medaka.";
DNA Cell Bicl. 17:835-847(1998).
-!- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING CALCIUM AND PROSPHOLIFID (BY SHILLARITY).
-!- SIMILARITY: GENTAINS 4 ANNEXIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 AA; 35424 MW; D2EED32C8676777D CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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SEQUENCE FROM N.A.
MEDLINE=990:5617; PubMed=9809745;
Osterloh D., Wittbrodt J., Gerke V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
MEDLINE=99025617; PubMed=9809745;
                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00151; annexin; 4.
PRINTS; PR06196; ANNEXIN.
ProDom; PD060143; Annexin; 4.
SMART; SM00335; ANX; 4.
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                                                                                                                                                                                                                                   EMBL; Y11252; CAA72122.1; -. HSSP; P13214; 1ANN.
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Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDYKKALLLLCG 317
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InterPro; IPR001464; Annexin.
                                                                PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
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                                                                                                                       PROSITE; PS00223; ANNEXIN; 4
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                   InterPro; IPR006031; XYPPX.
                                  Pfam; PF00191; annexin; 4.
Pfam; PF02162; XYPPX; 9.
                                                                                                                                                                                                           Matches 173; Conservative
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                                                                                                                                                                                           Similarity
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                                                                                                                                         SEQUENCE
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 NKVYKAEYGKTLEDSISSDTSGHFRRLLVSLCQGNRDERETVDISLAKQDAQKLYAAGEN 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 305
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                                                  ONE BINDING SITE FOR
cterization and developmentally regulated expression of four
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n; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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S.A., Olson E.S., Halpern M.E.;
ebrafish Annexin | Gene Family.";
Res. 0.0-0(2003).
AY178802; AA20276.1; -.
:0005509; F:calcium ion binding; IEA.
:0005544; F:calcium-dependent phospholipid binding; IEA.
                                                                                                                                                     :0005509; F:calcium ion binding; IEA.
:0005544; F:calcium-dependent phospholipid binding; IEA.
ro; IPR001464; Annexin.
ro; IPR00191; xYPPX.
PF00191; annexin; 4.
PF00162; XYPPX; 15.
                                                                                                                                                                                                                                                                                                                                                                                                           54.1%; Score 866; DB 13; Length 508; 55.6%; Pred. No. 3.6e-54; tive 51; Mismatches 89; Indels
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-2003 (TrEMBLrel 24, Last sequence update)
-2003 (TrEMBLrel 25, Last annotation update)
            ns in the killifish medaka.",
11 Biol. 17:835-847(1998)
MAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ON:
LCIUM AND PHOSPHOLIPID (BY SIMILARITY).
MILARITY: CONTAINS 4 ANNEXIN REPEATS.
MILARITY: CONTAINS 4 ANNEXIN REPEATS.
P79134; IAVC.
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                                                                                                                                                                                                                                                                ; PD000143; ANNEXIN.
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175; Conservative
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axID=7955;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 NTPAYFAERLHKAMQGAGTKDRTLIRIMVSRSELDMLDIRQEYLRLFGKSLYTHISGDTS
                                                                                                                                                                                         6 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                              Gaps
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Seville R.A., Nijjar S., Barnett M.W., Jones B.A.;
"Annexin 4 (Xanx-4) has a role in the development of the pronephric tubules in Xenopus laevis.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- DOMAIN: A PARR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 4 ANNEXIN FAMILY.
-!- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
EMBL, AV039235; AAK83461.1;
-- SIMILARITY: CONTAINS GOODS STATEMENTS.
EMBL, AV039235; P.Calcium Joh binding; IEA.
GO, GO:0005544; F.calcium dependent phospholipid binding; IEA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                              .
                                                                 Length 485;
                                                                                                                           89; Indels
485 AA; 51461 MW; 59D4EE05C4FA253C CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                             53.9%; Score 862; DB 13; 54.9%; Pred. No. 6.6e-54;
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MEDINE=22388257, PubMed=12477932;

MEDINE=22388257, PubMed=12477932;

MILLINE=22388257, PubMed=12477932;

MILLINE=22388257, PubMed=12477932;

MILLINE=22388257, PubMed=12477932;

MILLINE=2388257, PubMed=12477932;

MILLINE R. P., Colling F. S., Wagner L., Schemen C.M., Schuler G.D.,

MILSTON R. P., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,

MILLINE R. P., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,

MILLINE R. P., Jordan H., Moore T., Max S. I., Wang J., Hong L.,

MILLINE R. P., Max D. M., Poeters G.J., Abramson R. D., Scheetz T. E.,

MILLINE S. J. Ioquellano N.A., Peters G.J., Abramson R. D., Mullahy S.J.,

MILLINE S. Morley K. C., Hale S., Garcia A. M., Gay L.J., Hulyk S.W.,

MILLINE S., Worley K. C., Hale S., Garcia A. M., Gay L.J., Hulyk S.W.,

MILLINE S., Morley R. M., Sodergren E.J., Lu X., Gibbs R. A.,

Millialon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R. A.,

Milling M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Milling M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Milling M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Milling M., Madan J.W., Green E.D., Myers R.M., Butterfield Y.S.,

Milling M. I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                   309 SRAYKTEFQKTLEEAIRSDTSGHFQRLLISLSQGNRDESTNVDMSLVQRDVQELYAAGEN 368
                                                                                                                                                                                                                                                                                                                     RGTITAASGFDPLRDAEVLRKAMKGFGTDEQAIIDCLGSRSNKQRQQILLSFKTAYGKDL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                126 KQVYEEEYGSSLEDDVVGDŢSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL
                                                                                                                                                                                                             KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                                                                                                                                                                                                                                                                                                SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eracuyganio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg E.;
Submitted (TUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AR178798; AR020272.1; -.
EMBL; BC054622; AAH54622.1; -.
GO; GO:0005509; F:calcium ion binding; IEA.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Farber S.A., Olson E.S., Halpern M.E.; "The Zebrafish Annexin Gene Family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                   GDYKKALLLLCGEDD 320
                                                                                                                                                                                                                                                                                                                                                                                                                          GDYRKILLKICGGND 503
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TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FRCM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7955;
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                                                                                                                                                                                                                 66 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
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                                                                                                                                                                                                                                                                                                    KOVYEERYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 185
                                                                                                                                                                                                                                                                                                                              KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 305
                                                                                                                                  65
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                                                                                                                                                                                                                                                                                                                                                                                                             SRPAYFAERLYKSMKGLGTDDXTLIRVMVSRCEIDMLEIRCEFKKMYGKSLHSFIKGDCS
                                                                                                                              .6 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                                                         RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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                                                 Length 321;
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                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          503 AA; 54079 MW; 33F3471EE21A0D32 CRC64;
      5C28CAFAAC17687D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last annotation update)
                                            53.7%; Score 859; DB 13; L
54.3%; Pred. No. 6e-54;
ive 55; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
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-!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-!- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
EMBL; BC012875; AAH12875.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              503 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005635; C:nuclear membrane; ISS
GO; GO:0005654; C:nucleoplasm; ISS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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Pfam; PF00191; annexin; 4.
      35801 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDYKKALLLCGEDD 320
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GDYRKVLLKLCGGED 321
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                                                                  Best Local Similarity 54.3
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI:108481; Anxall.
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      321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Best Local 9
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Q921F1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 VYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAG-IDEAQVEQDAQALFQAGELK 186
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                                                                                                                     SSLEDDVVGDTSGYYQRMLVVLLQANRDPDAG-IDEAQVEQDAQALFQAGELKWGTDEEK 193
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                 80
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                                                                                                                                       201 FITLCTRSATHLMRVFEEYEKIANKCIEDSIKSETHGSLEEAMLTVVKCTRNVHSYFAE
                                                                                                                                                                                                                                                           254 TLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSGDYKKALL
                                                                                                                                                                                          194 FITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRSIPAYLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ANNEXIN FEPERTS.
-!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-!- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
EMBL; AF417637; AAL13308.1; --
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom, PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
PROSIT: S500223; ANNEXIN; 4.
Annexin; Calcium, Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6; Length 327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   White A.H., Wallis G.A.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 327 AA; 36787 MW; 2EB178E13738CF22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.3%; Score 837.5; DB 6 55.9%; Pred. No. 2.2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 175; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                314 LLCGED 319
                                                                                                                                                                                                                                                                                                                                                                   321 NLVGTD 326
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Bos taurus (Bovine)
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                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 22
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                                                                                                                                                                                                                                                                                                                                                                                                          86 KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 FDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSELT 74
                                                                                                                                                                                                                                                 65
                                                                                                                                                                                                                                                                                99
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                                                                                                                                                                                                                                                                    Gaps
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ia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
PaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.6%; Score 841.5; DB 11; Length 327; 57.8%; Pred. No. 1.1e-52; ive 49; Mismatches 79; Indels 1;
     :0005544; F:calcium-dependent phospholipid binding; IEA
                                                                                                                                                                              Length 321;
                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        berg R.;
ted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PE; PS00223; ANNEXIN; 4.
VCE 327 AA; 36724 MW; 56DB9CFAFA8C2B21 CRC64;
                                                                                                                                         321 AA; 35634 MW; 72F81AD1E753B29D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                            53.2%; Score 855; DB 13; 53.2%; Pred. No. 1.2e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327 AA
                                                                                                                                                                                                               62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                     ro; IPR001464; Annexin.
PF00191; annexin; PR00196; ANNEXIN.
; PD000143; Annexin; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00191; annexin; 4.
; PR00196; ANNEXIN.
; PD000143; Annexin; 4.
SM00335; ANX; 4.
                                                                                           SM00335; ANX; 4
E; PS00223; ANNEXIN; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22,
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                                                                                                                                                                                                                 166; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07 GDYRKILLELCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDYKKALLLLCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                r to annexin A8
                                                                                                                            etical protein.
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Similarity

ICE FROM N.A.

-2003

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(TrEMBLrel.
                  01-MAR-2003
01-MAR-2003
01-OCT-2003
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01-DEC-2001
01-OCT-2003
Annexin A7.
                                                                                 Annexin A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                      ANXA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 25
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ACCOORDING TO THE PROPERTY OF 
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                    246
                                                                                                    306
                                                                                                                       194 CGTDEMKFITILCTRSARHLMRVFEEYEKIANKSIEDSIKSETHGSLEEAMLTIVKCTRN 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 VYEBEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAG-IDEAQVEQDAQALFQAGELK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGPQIEETIDRETSGNLEQLLLAVVKSIRS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 TVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73
                  WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
                                         247 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cheng W., Tsao F.H.C.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AF012745; AAD01508.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eut
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 4.
SEQUENCE 327 AA; 36680 MW; 1815B77B6BE50AB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89;
                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.5%; Score 823.5; DB 6 55.9%; Pred. No. 2.2e-51;
                                                                                                                                                                                                                                                                                                                                   327 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                    DYKKALLLCGED 319
                                                                                                                                                                                                               DYKKALLLLCGED 319
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Best Local Similarity 55.9
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYKNALLSLVGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Annexin VIII.
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                187
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                                                                                                                                                                                                                                                                                           RESULT 23
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323 AA.

PRT;

PRELIMINARY;

RESULT 24 QBC1X9 ID QBC1X9

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KOVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length CDNs."; Nature 420:563-573 (2002).
EMBL; AK090055; BAC41070.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 KWGTDEDKFTEVLCLRSFPOLKLTFDEYRNISOKDIEDSIKGELSGHFEDLLLAIVHCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1201378; Arxa3.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA
InterPro; IPR001464; Annexin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9F69F57BCFAC6A85 CRC64;
                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.6%; Score 809; DB 11; 49.5%; Pred. No. 2.4e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63; Mismatches
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Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                       TISSUE=Kidney;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 AA; 36356 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00191; annexin; 4. PRINTS; PR00196; ANNEXIN. ProDom; PD000143; Annexin; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 4.
SEQUENCE 323 AA; 36356 MW;
23,
23,
25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 19, 1
(TrEMBLrel. 19, 1
(TrEMBLrel. 25, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDYKKALLLLCGEDD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDYRTVLLKICGEDD 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                  (TrEMBLrel.
                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                   SEQUENCE FROM N.A.
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LUEG (MAY-2001) to the EMBL/GenBank/DDBJ databases.

MAIN: A PAIR OF ANYEXIN REPEATS MAY FORM ONE BINDING SITE FOR ALCIUM AND PHOSPHOLIPID (NILLARITY).

IMILARITY: BELONGS TO THE ANNEXIN FAMILY.

IMILARITY: CONTAINS 4 ANNEXIN REPEATS.

BROOB997; AAH08997.1; -.
NCE FROM N.A.
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329170; \$29170.

#GI:88031; Anxa7.|
>:0005509; F:calcium ion binding; IEA.
>:0005544; F:calcium-dependent phospholipid binding; IEA.
Pro; IPR001464; Annexin.

PF00191; annexin; 4. S; PR00196; ANNEXIN. n; PD000143; Annexin; 4

SM00335; ANX; 4. FE; PS00223; ANNEXIN; 4. In; Calcium; Calcium-binding; Calcium/phospholipid-binding;

463 AA; 49909 MW; D2D5FF652E85F6ED CRC64; ČE.

Gaps 48.4%; Score 774; DB 11; Length 463; 47.5%; Pred. No. 1.4e-47; i.ye 68; Mismatches 99; Indels 151; Conservative ch al Similarity

1 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL 60

61 FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120

ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF 180 121

181 QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV 240

141 VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 300

101 KGDTSGDYKKALLLLCGE 318

March 25, 2004, 08:06:21 49 secs

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Result
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Maximum Match 100%
Listing first 100 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
1488.5
1488.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                  1600
1600
1600
1600
1600
1597
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match
100.0
1100.0
1100.0
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Best Local (
                                                                                                                                                                                                                                                                                                            This polypeptide exhibits strong anticoagulant activities and is useful for the treatment and prevention of e.g. thrombosis or disseminated intravascular coagulation in the brain, heart and peripheral blood vessels, such as cerebral and myocardial infarction. It has no
                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                        antigenicity against man and can be produced in large amts. using recombinant methods. (Updated on 10-MAR-2003 to add missing CS field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003)
                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page ?; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant placental coagulation inhibitor - useful for the prevention and treatment of thromboses or disseminated intravascular coagulation.
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                                                                                    into a host animal, in conjugation with eg keyhole limpet haemocyanin, and the B-cells from immunised hosts are then fused with myeloma cells. The resultant hybridomas (VAA-8 and VAA-9) produce Abs specific to VAC-alpha. Abs can be used as immunoassay reagents to detect VAC proteins, affinity ligands for protein purificm. and as medicaments for binding and/or neutralising VAC proteins in vivo. See also AAN91354 and EP-181465. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 20-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
10-MAR-2003
                                                   Sequence
                                                                                                                                                                                         This vascular anti-coagulating protein (VAC)-alpha is used in the preparation of monoclonal antibodies (MAbs). The VAC-alpha is injected
                                                                                                                                                                                                                             Disclosure; Fig 1; 11pp; German.
                                                                                                                                                                                                                                                                                                         WPI; 1989-293724/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vascular anti-coagulating
                                                                            field)
                                                                                                                                                                                                                                                        hybridomas
                                                                                                                                                                                                                                                                    Monoclonal
                                                                                                                                                                                                                                                                                             N-PSDB; AAN91353
                                                                                                                                                                                                                                                                                                                                  Gunther
                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vascular anti-coagulating proteins; hybridomas; B-cells; myelomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUL-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP91953 standard; protein; 320
                                                                                                                                                                                                                                                                                                                                                           (BOEH ) BOEHRINGER INGELHEIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                      antibodies to vascular anti-coagulating proteins - producing such antibodies.
100.0%; ilarity 100.0%; Conservative 0
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           Score 1600; DB 1;
Pred. No. 1.3e-134;
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                                                                                                This sequence, or a fragment of it, is used in the construction of hybrid phospholipid-binding proteins (PBP) comprising at least one lipocortin phopholipid binding domain (PBD), e.g. of PAP-I, joined to a gladomainless vitamin K-dependent protein, e.g. protein C or activated protein C. See AAQ12680-81 for such examples. See also AAQ12678-81. Updated on 25-MAR-2003 to correct PA field.)
                                                                                    Sequence 320
                                                                                                                                                                       Disclosure; Fig 7; 57pp; English.
                                                                                                                                                                                        Recombinant prodn. of hybrid phospholipid-binding proteins - comprising lipocortin phospholipid-binding domain and vitamin=K-dependent protein.
                                                                                                                                                                                                                                                             Foster DC;
                                                                                                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                   29-DEC-1989;
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                                                                                                                                                                                                                                                                                                                                                               WO9109953-A.
                                                                                                                                                                                                                                                                                                                                            11-JUL-1991.
                                                                                                                                                                                                                                                                                                                                                                                                        gla-domain;
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                              Phopholipid;
                                                                                                                                                                                                                                                                                                                                                                                                                                      PAP-I.
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30-SEP-1991
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DB; AAQ12679.
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            MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
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                                            Conservative
                                                                                    Ä,
                                                                                                                                                                                                                                                                                                                                                                                                          binding protein; lipocortin; domain; vitamin
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(first entry)
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                                                     100.0%;
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                                          Score 1600;
Pred. No. 1.3
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                                                                                                                                                    Bifunctional fusion protein useful for the detection
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                                                                                                                                                                                                                                  09-OCT-1997;
                                                                                                                                                                                                                                                     09-OCT-1998;
                                                                                                                                                                                                                                                                        22-APR-1999
                                                                                                                                                                                                               (REGC ) UNIV
                                                                                                                                                                                                                                                                                          WO9919470-A2
                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                       asymmetric distribution; plasma
                                                                                                                                                                                                                                                                                                                                                                                             S65T GFP variant/hAnnexin V protein
                                                                                                                                                                                                                                                                                                                              Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                apoptotic cell detection.
                                                                                                                                                                                                                                                                                                                                                                            GFP; green fluorescent
                                                                                                                                                                                                                                                                                                                     domo sapiens.
                                                                                                                                                                                                                                                                                                                                                                   fluorescent intensity;
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                                                                                                                                                                                                              CALIFORNIA
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                                                                                                                                                                                                                                 97US-00948276.
                                                                                                                                                                                                                                                    98WO-US021444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                  entry
                                                                                                                                                                                                                                                                                                                                                    protein; annexin; fusion protein; apoptosis;
anionic phospholipid binding affinity;
n; plasma membrane phospholipid;
                                                                                                                                                    of.
                                                                                                                                                    apoptotic cel
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This sequence represents an example of a protein of the invention. The proteins are bifunctional Aequorea victoria green fluorescent protein (GFP)-annexin fusion proteins, where the GFP and annexin moieties proteins are useful fluorescent intensity and anionic phospholipid bindir greater or equal fluorescent intensity and anionic phospholipid bindir of affinity, respectively, than do the corresponding unfused GFP and annexin of proteins. An early manifestation of apoptosis is the loss of the companies of the co

Claim 2; Page 14-15; 23pp; English.

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SXS
RESULT 5
AAX/84788
AID AAAX/84788
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AC AAX/8
DT 08-2
DT 08-2
DXX Annir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Annexin; phospholipid; antithrombotic; antitumor; antiinflammatory; coating; thrombogenic biomaterial; labelling compound; negative charge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY84788
                                                              Chemical structure having affinity for phospholipid comprises chemical platform comprising six residues supporting set of chemical functions that are capable of binding to phospholipid.
                                                                                                                                                                                                                                                                                                                                                                    02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                07-APR-2000
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                                                                                                                                                            WPI; 2000-320664/28
                         Claim
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UNIV CURIE PARIS VI P & M.
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Pred. No. 1.3e-134;
Mismatches 0;
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Best Local S
Matches 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 320
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                                                                                                                                                                                                          ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
                                                                                                                                                                                                                                                            PGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE
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                                                                                                                                QAGELKWGTDBEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
                                                                                                                                                                                      ELKAIKQVYEBEYGSŠLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
                                      VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
                                                          KGDTSGDYKKALLLLCGEDD
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pred. No. 1.3e-134;
0; Mismatches 0;
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RESULT 6
ABG31220
Human; annexin V; delta RACK; delta protein kinase C; deltaPKC; VI domain; vasotropic; cerebroprotective; deltaV1-1; deltaV1-2; RACK; pseudo-delta RACK; pseudo-delta receptor for activated C-kinase; deltaV1-5; PKC; protein kinase C; signal transduction; cell growth; gene expression; ion channel activity; translocation; hypoxia; stroke;
                                                                                                                                                                                                                                                         Human annexin V, containing a delta RACK binding site
                                                                                                                                                                                                                                                                                         05-NOV-2002
                                                                                                                                                                                                                                                                                                                                             ABG31220
                                                                                                                                      Homo sapiens
                                                                                                            WO200257413-A2
                                                                                                                                                                ischaemic damage;
                          18-JAN-2001; 2001US-0262060P
                                                      09-NOV-2001; 2001WO-US047556
 (STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                               standard;
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                                                                                                                                                                   creatine kinase.
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RESULT 7
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                                        24-OCT-2003
25-MAR-2003
01-NOV-1989
             anticoagulant PP4 protein
                                                                                                 AAP90053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   turn appears due to binding of the activated isozymes to the specific anchoring molecules (RACKs). Peptides that mimic either the PKC-binding site on RACKs or the RACK-binding site on PKC are isozyme specific translocation inhibitors of PKC. The disclosed peptides are useful in activating or inhibitors of PKC. The disclosed peptides are useful in deltaPKC agonists or antagonists are useful in reducing, enhancing or protecting against damage to cells or tissues due to ischaemic or hypoxic event caused by stroke. Acute administration of the peptides, conjugated to a carrier peptide or a Tat-derived peptide, protected hearts against data indicate that in an intact heart, inhibition of deltaPKC conferred greater than 50% protection against ischaemic damage. The sequence presented is human annexin V, which contains a delta RACK binding site
                                                                                                                        AAP90053 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention discloses peptides comprising deltaV1-1, deltaV1-2, pseudo-delta receptors for activated C-kinase (RACK), deltaV1-5 or their derivatives or fragments. Protein kinase C (PKC) is a key enzyme in signal transduction involved in a variety of cellular functions including cell growth, regulation of gene expression and ion channel activity. The localisation of different PKC isozymes to different areas of the cell in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 45; Page 64-65; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New delta protein kinase C peptide for reducing or enhancing cells or tissues exposed to ischemic or hypoxic event caused
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protecting tissue from damage due to ischemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                   VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVGRSEIDLFNIRKEFRKNFATSLYSMI
                                                                                                                                                                                             KGDTSGDYKKALLLLCGEDD 320
                                                                                                                                                                                                                   KGDTSGDYKKALLLLCGEDD 320
                                                                                                                                                                                                                                             VKSÍRSÍPAYLAETLYYANKGAGTDDHTLÍRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
                                                                                                                                                                                                                                                                                                       QAĞBLKWĞTDEEKFİTİFĞTRSVSHLRKVFDKYMTİSGFQİBETIDRETSĞNLEQLLLAV
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Pred. No. 1.3
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Annexin V; thrombocyte; carrier; thrombus;
                          Annexin V/urokinase fusion protein.
                                                           25-OCT-2000
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Query Match 99.8
Best Local Similarity 99.7
Matches 319; Conservative
AAY92930 standard; protein; 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coagulation at the thromboplastin stage. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of anticoagulant PP4 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA sequence encoding anticoagulant PP4 protein protein, vectors, antibodies, etc., useful therapeut
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                                                                                                                                                                                                                                                                                          QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
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                                                                                                    KGDTSGDYKKALLLLCGEDD
                                                                                                                                             KGDTSGDYKKALLLLCGEDD
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99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1597; DB 1;
Pred. No. 2.5e-134;
1; Mismatches 0;
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(first entry)

thrombolytic;

fusion prote

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RESULT 9
AAP82317
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AC AAP8
XC
DT 25-N
DT 13-N
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        urokinase; insect
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Annexin V, which has high affinity for active thrombocytes, is used as a carrier molecule to build a thrombus-targeting thrombolytic fusion protein. The protein (this sequence) is the result of expression of a fusion gene comprising the Annexin V gene and a low-molecular urokinase gene, in insect cells. The Annexin V-scu-PA-32 fusion protein, expressed in insect cell strain Tn-5B1-4, has high affinity for active thrombocytes and has the fibrinolytic activity of urokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wux,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New thrombolytic fusion protein for fusion of Annexin V and urokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 600 AA;
PAP-I isolated from biological fluid, used
                                                                           AAP82317
                                  25-MAR-2003
                       13-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                   FGRDLLDDLKSELTGKFEKLIVALMKÞSRLYDAYELKHALKGAGTNEKVLTEI I ASRTÞE
                                                                                                                                                                                                                                                                                                                   QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNÜEQLÜLAV
                                                                                                                                                                                                                                                              ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVBQDAQALF
                                                                                                                                                                                                                                                                           ELRAIKQVYEBEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVI3QDAQALF
                                                                                                                                                   KGDTSGDYKKALLLLCGEDD
                                                                                                                                                                           VKŚIRŚIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
                                                                                                                                                                                          VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMYSRSEIDLFNIRKEFRKNFATSLYSMI
                                                                                                                                                                                                                                 QAGELKWGTDBEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGN1EQ11LAV
                                                                            standard;
                                                                                                                                  KGDTSGDYKKALLLCGEDD
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                       (revised)
(first entry)
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                                                                            protein;
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                                                                                                                                                                                                                                                                                                                                                                                               Score 1597; DB 3;
Pred. No. 5.8e-134;
1; Mismatches 0;
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    as anticoagulant.
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RESULT 10
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The protein does not contain a leader peptide sequence, indicating that PAP-I is probably not constitutively secreted. The Met residue is removed at in a post-translational event and the newly formed NH2-terminal Ala residue is blocked by acetylation. It binds to phospholipid and inhibits phopholipase A2. The protein can substitute heparin or other anticoagulants in the treatment of disseminated intravascular coagulation, deep vein thrombosis, or other disorders. It also has antiinflammatory properties. (Updated on 25-MAR-2003 to correct PA field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-FEB-1987;
05-JUN-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human proteins having anticoagulant and antiinflammatory activity isolated from biological fluids by anion-exchange chromatographic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAN82107
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   320
                                                                                                                                                                                                                                                                                                                             FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
                                                                                                                                    VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
                                                                                                                                                                                      QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV 240
                                                                                                                                                                                                                         ELRAIKQVYBBBYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDBAQVBQDAQALF
                                                                                                                                                                                                                                       ELRAIKQVYBBEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF 180
                                                                                                                                                                                                                                                                           FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEITASRTPE 120
                                                                                                                   VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
                                                                                                                                                                     QAĞELKWGTDEEKFITIFGTRSVSHFRKVFDKYMTISGFQIEETIDRETSĞNLEQLLLAV
                                                                             KGDTSGDYKKALLLLCGEDD 320
                                                                KGDTSGDYKKALLLLCGEDD
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87US-00059355
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99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                              Score 1596; DB 1
Pred. No. 3e-134;
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                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 320;
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AAR26276

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RESULT 11
AAR41021
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AC AAR41
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Best Local
                           AAR41021
         AAR41021;
                                                                                                                                                                                                                                                                                                                                                                     The sequence given is the amino acid sequence of CPB-I. CPB-I was used within a method which involved adding basic amino acids to it which resulted in its stabilisation. This lead to the production of CPB-I which keeps its activity when it is frozen, molten or has been processed by several procedures. (Updated on 10-MAR-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stabilisation of CPB-I for drug compsn. - by adding selected from lysine, arginine and/or ornithine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAR-2003
04-FEB-1993
                                                                                                                                                                                                                                                                                                                                                         Sequence 319
                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 2; 4pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-288937/35.
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                                                                                                                                                                                                      122 LRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQ 181
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                                                                                                                                                  AGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVV
                          standard; protein; 319 AA
                                                                         GDTSGDYKKALLLLCGEDD
                                                                                                            KSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIK 300
                                                                                                                         KSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSBIDLFNIRKBFRKNFATSLYSMIK 301
                                                                                                                                                                AGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVV
                                                                                                                                                                                         LRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQ
                                                                                                                                                                                                                               GRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE
                                                                                                                                                                                                                                             GRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE
                                                                                           GDTSGDYKKALLLCGEDD 320
                                                                                                                                                                                                                                                                     AQVLRGTVTDFFGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLF
                                                                                                                                                                                                                                                                                      AQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLF
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                         AA;
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(first entry)
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                                                                                                                                                                                                                                                                                                                          99.7%;
                                                                                                                                                                                                                                                                                                                 0;
                                                                          319
                                                                                                                                                                                                                                                                                                              Score 1595; DB 2; : Pred. No. 3.7e-134; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                  Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                basic aminoacid
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RESULT 12
ABG3250
ID ABG32
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AC ABG32
XX
DT 29-NC
XX
XX
DE Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
               Human CPB-1
                                               29-NOV-2002
                                                                                                                   ABG32550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein kinase C (PKC) and is useful in the treatment of malignant tumours caused by abnormal activation of PKC. CPB-I is extracted from human or animal organs and may be applied intravenously, orally,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calphobindin I (CPB-I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intramuscularly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein kinase C inhibitor effective against malignant tumours - con (opt. recombinant) calphobindin I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-299558/38
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(KAGA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-1992;
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ilarity 100.0%;
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calcium/phospholipid binding protein; polyhydric alcohol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eye drops for treating e.g. corneal diseases, contain CPB-I and polyhydric alcohol with specific carbonyl value, without umpleasant irritation upon dropping but with satisfactory long-term storability.
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Human Protein P08758, SEQ ID NO 893.
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                                                                                                                                                                                                                                                                                                                                                  GRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEI:(ASRTPEE
                                                                                                                                                                                                                                                                                                          LRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQ 181
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GRDLLDDLKGBLTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 121 AQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLF AQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLF

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al Similarity 319; Conserva

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Score 1595; DB 7; I Pred. No. 3.7e-134; 0; Mismatches 0;

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CC derivative or allelic variation of the mucleic acid sequence. Also comprising the vector comprising the novel polynucleotide, a host cell claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal compound that regulates the expression of the polynucleotide sequence the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal compound that regulates the activity of one or more of the polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound which regulates the compound that regulates the activity of one or more of the polynucleotides given in the polynucleotides or identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more completed that regulates the compound that regulates the its activity is useful for preparing a medicament for treating pain and a pharmaceutical composition comprising the one or more completed that polypeptides or their antibodies. The polynucleotide or the compound that compound that polypeptides or their antibodies. The polynucleotide or the compound that compound provides that polypeptides or the provide that polypeptides or the provide that polypeptides or the provide that compound that compound that polypeptides or the provide that polypeptides or the compound that polypeptides or the provide that polypeptides or the compound that compound that polypeptides or the provide that polypeptides or the provide that polypeptides or the provide that polypeptides or the provide that polypeptides or the provide that polypeptides or the provide that polypeptides or t
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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GENBANK; P08758.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention discloses a composition comprising two or more isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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(FARB )
    Sequence
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CC claimed are a vector comprising the novel polynucleotide, a host cell CC comprising the vector, a method for identifying a nucleotide sequence CC which is differentially regulated in an animal subjected to pain and a CC kit to perform the method, an array, a method for identifying an agent CC that increases or decreases the expression of the polynucleotide sequence CC that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially CC expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound for identifying a compound useful in the specification, a method for identifying a compound useful in treating and a nimal and former of the polypeptides given in the specification, a method for identifying a compound useful in treating animal and a name animal compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in treating the compound useful in the compound useful in the compound useful in the compound useful in the compound useful in the compound useful in the compound useful 
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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28-MAR-1987; 28-MAR-1987; 28-MAR-1987; 04-NOV-1987;

87DE-03710309. 87DE-03710364. 87DE-03710430.

26-MAR-1988;

88WO-EP000266

Hauptmann R, Falkner E, 1

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                                                                                                                                                                                     06-OCT-1988
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(first entry)
  /label= tryptic peptide 30. .45
                                           Location/Qualifiers
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Pred. No. 4.6e-134;
2; Mismatches 0;
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The DNA is produced by determining the amino acid sequence of isolated and highly purified VAPs, constructing DNA probes on the basis of this sequence, using the probes to search through suitable cDNA libraries, isolating cDNA that hybridises with the probes, by inserting the cDNA into a suitable vector, and using the vector to transform a host organism. The posn. of the AA sequences used to construct the probes are given in FT. VAC-alpha has anticoagulant activity under certain conditions, but loses this activity in the event of severe bleeding. It acts by inhibiting conversion of factor X to factor Xa and conversion of prothrombin to thrombin. It is structurally related to lipocortin I prothrombin to thrombin and lipocortin I (Cell, 46, 191/120, 1986) and has similar antiinflammatory and phospholipase inhibitory activity. (Updated on 25-MAR-2003 to correct PR field.)
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Falkner E,
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                                                                                                                                                5/1-5/2; 183pp; German.
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correct PA field.)

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RESULT 17
AAR11910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                           25-MAR-2003
10-MAR-2003
    This vascular
                                    Anticoagulants contg. annexin or its analogues and derivs. treat tumours and to reduce metastases.
                                                                      WPI; 1991-149572/21.
                                                                                                                                                    11-NOV-1989;
                                                                                                           (BOEH ) BOEHRINGER INGELHEIM
                                                                                                                                  11-NOV-1989;
                                                                                                                                                                                            DE3937607-A
                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                     Annexin; anticoagulant; tumour metastasis; fibrin; cancer
                                                                                                                                                                                                                                                                                           Vascular anticoagulant protein.
                                                                                                                                                                                                                                                                                                                                                                          AAR11910 standard; protein; 320 AA
                                                                                                                                                                         16-MAY-1991
                                                                                                                                                                                                                         Misc_difference
                                                                                                                                                                                                                                                                                                                                                           AAR11910;
                                                                                                                                                                                                                                                                                                                                                                                                                                301
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                   Page 11; 17pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                       KGDTSGDYKKALLLLCGEDD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKS IRS IPAYLAETLYYAMKGAGTDDHTL IRVMVSRSEIDLFNIRKBERKNFATSLYSMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKSIRSIPÄYLÄETLYYÄMKGÄGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFÄTSLYSMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELRATKÓVYEEEYGSSLEDDVVGDTSGYYÓRMLVVLLÓANRDPDAGIDEAÓVEÓDAÓALF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQBISAAPKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 AA;
                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
anticoagulant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                89DE-03937607
                                                                                                                                                  89DE-03937607
                                                                                                                                                                                                           Location/Qualifiers
22. .22
/label= Glu, Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.6%;
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Pred. No. 4.6e-1
2; Mismatches
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(VAC) comprises an

annexin.

ij

The sequence given is the amino acid sequence of CPB-1. CPB-1 was used within the method of the invention which involved adding saccharides t

Disclosure; Page 2; 4pp; Japanese.

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ARESULT 18
AAR26180
ID AAR26
XX
AC AAR26
XY
DT 10-MA
DT 04-FE
XX
XX
DT CFB-1
XX
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Best Local Similarity
Matches 319; Conserv
                                                 Stabilisation of CPB-1 for drug compsn. - contains saccharide from glucose, glucosamine, xylose, saccharose and/or dextran.
                                                                                           WPI; 1992-288938/35
                                                                                                                                                      28-NOV-1990;
                                                                                                                                                                                                        17-JUL-1992
                                                                                                                                                                                                                                                                                      CPB-1; saccharides; stabilisation; antihemagglutination;
                                                                                                               (KOWA ) KOWA CO LTD.
(KAGA ) KAGAKU OYOBI KESSEI RYOHO
                                                                                                                                                                                28-NOV-1990;
                                                                                                                                                                                                                                 JP04198196-A
                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                 corneal
                                                                                                                                                                                                                                                                                                                                             10-MAR-2003
04-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                   AAR26180;
                                                                                                                                                                                                                                                                                                                                                                                                       AAR26180 standard; protein; 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          formulated with auxiliaries, carriers and/or stabilisers for prevent tumour cell metastasis: Admin. is by injection, in a pref. dosage of -0.05 mg/kg, or using a topical formulation in a dosage of 0.25-10 m ml soln. or log gel. (Updated on 10-MAR-2003 to add missing Os field (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 320 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGDTSGDYKKALLLLCGEDD 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLA
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                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                      90JP-00328287
                                                                                                                                                                              90JP-00328287
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99.7%;
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Pred. No. 4.6e-134;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      it which resulted in its stabilisation. The saccharide was pref. glucost glucosamine, xylose, saccharose or dextran. This lead to the production of CPB-I which kept its activity when it had been processed by several treatments. CPB-I can be used as a medicine for antihemagglutination, dermal and corneal diseases. (Updated on 10-MAR-2003 to add missing OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 319 AA;
                                                                                                                                                                                                                                                                                                                                                  AAB50864;
                                                                                                                                                                                                                                                                                                                                                                        AAB50864 standard; protein;
                                                                                                                                                                                                                                                                                                                           16-MAR-2001
                                                                                                                                                   01-JUN-1999;
                                                                                                                                                                         25-MAY-2000; 2000WO-US014324
                                                                                                                                                                                                                      WO200073332-A1
                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                    transplant rejection.
                                                                                                                                                                                                                                                                               Human;
                                                                                                                                                                                                                                                                                                      Modified human annexin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 318; Conserv
Claim 15; Page 33-35; 39pp; English
                                                                                                     Tait JF,
                                 Novel modified annexin useful for imaging vascular thrombi and apoptosis, has N-terminal chelation site comprising amino acid extension which
                                                                                                                              (WIW)
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                                                                                 2001-080465/09.
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                                                                                                                                                                                                                                                                              annexin; chelation site; nuclear imaging; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQ
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                                                                       AAC91369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                GDTSGDYKKALLLLCGEDD 320
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                       glycine and a cysteine residue.
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99.7%;
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Pred. No. 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; annexin; chelation site; nuclear imaging; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                       WO200073332-A1
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transplant rejection
        N-PSDB; AAC91370
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                            WPI; 2001-080465/09.
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Pred. No. 1.le-133;
0; Mismatches 1;
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RESULT 21
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Best Local
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                                                 25-MAY-2000; 2000WO-US014324
                                                                            07-DEC-2000
                                                                                                                           Homo sapiens
                                                                                                                                                                                   Modified human annexin, SEQ ID NO: 2.
                                                                                                                                                    transplant rejection
                                                                                                                                                                                                                                                                 AAB50863 standard; protein; 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombi or apoptosis which is associated with response to a chemotherapeutic agent or with rejection as a result of transplantation. The modified annexin can effectively chelate a radionuclide and retain annexin bioactivity. It can be readily prepared in high radiochemical yield and with high radiochemical purity. In contrast to conventional conjugation chemistries that provide a distribution of conjugation products, the modified annexin has a single chelation site remote from the site of biological activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Page 37-38; 39pp; English
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99.7%;
                                                                                                                                                        site; nuclear imaging; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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Pred. No. 1.1e-133;
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RESULT 22
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                          Human lipocortin-V; lambdaHLipo V-1; anti-inflammatory
    Homo
                                                                                  Human lipocortin-V
                                                                                                                                                                     AAP91363;
                                                                                                                                                                                                    AAP91363 standard; protein;
                                                                                                                            22-DEC-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombi or apoptosis which is associated with response to a chemotherapeutic agent or with rejection as a result of transplantat. The modified annexin can effectively chelate a radionuclide and reta annexin bloactivity. It can be readily prepared in high radiochemica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the site of biological activity
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                                                                                                                                                                                                                                                                                                                                                                                           VKSIRSIPAYLAETLYYÄNKGAGTDDHTLIRVMVSRSEIDLFNIRKEERKNEATSLYSMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
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99.7%;
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Pred. No. 1.1e-133;
0; Mismatches 1;
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RESULT 23
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Best Local Similarity
Matches 318; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lipocortin cpds. III, IV, V, arthritic, allergic, dermatologic, involving inflammatory processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human lipocortin-V was isolated from a lambda gt10 human peripheral blood lymphocyte cDNA library with rat lipocortin-V cDNA of lambda RLipo V-1 as probe. Lipocortins are anti-inflammatory agents and can be used to treat arthritic, allergic, dermatologic, ophthalmic, and collagen diseases. See also AAN90598, AAN90599, and AAP91362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wallner BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Fig 4; 32pp; English
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                                                                                 Nerve cell protecting
                                                                                                       CPB-1
                                                                                                                             18-JAN-1993
                                                                                                                                                    AAR25718;
                                                                                                                                                                         AAR25718 standard; protein; 319
                                                         Homo sapiens
                                    JP04173744-A
            22-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                       FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
                                                                                                                                                                                                                                                                                                                                                                           ELRATKÓVYEBBYGSSLEDDVVGDTSGYYORMLVVLLQANRDPDÁGIDEAQVEQDAQALF
                                                                                                                                                                                                                                                                                                                                                                                      ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
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99.4%;
                                                                                   agent; placenta
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Pred. No. 1.9e-133;
0; Mismatches 2;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 3; 5pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of human placenta derived coagulation inhibitor, CPB-1 - for preventing and treating senile dementia and brain vessel lesions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1992-255655/31.
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                                                                                                                                                                                                                                                         AQVLRGTVTDE PGEDERADAGTLRKANKGLETDEES ILTLLTSRSNAQRQEISAAFKTLE
                                                                                                                    AGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVV
                                                                                                                                                      ĹŔĀĬĸŎVŶĔĖĖŶĠĠĠĹĔĎĎVVĠĎŤŚĠŶŶŎŖMĹŸVĹĹQĀNRĎĖĎĀĠĬĎĔĀQVĔŎĎĀQĀLFQ
                                                                                                                                                                        LRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQ
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                                                                                                   AGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEET
              GDTSGDYKKALLLLCGEDD 320
                                                 ksirsipaylabtlyyankgagtddhtlirvmvskseidlenirkeerkneatslysmik
                                                                KSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMYSRSEIDLFNIRKEFRKNFATSLYSMIK
QDTSGDYKKALLLLCGEDD
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98.7%;
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                                                                                                                                                                                                                                                                                                              Score 1563; DB 2;
pred. No. 2.7e-131;
0; Mismatches 4;
     319
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RESULT GPP; green fluorescent protein; annexin; fusion protein; apoptosis; fluorescent intensity; anionic phospholipid binding affinity; asymmetric distribution; plasma membrane phospholipid; S65T GFP variant/hAnnexin V protein 13-JUL-1999 AAY13924 apoptotic cell detection Synthetic Aequorea victoria Homo sapiens. 24 standard; (first entry) protein; 319 \$

WO9919470-A2

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RESULT 25
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Mouse; ischaemia; compressive ischaemia;
                              Mouse ischaemic condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         affinity, respectively, than do the corresponding unfused GFP and annexin proteins. An early manifestation of apoptosis is the loss of the asymmetric distribution of plasma membrane phospholipids, which results in exposure of anionic phospholipids on the extracellular leaflet of the plasma membrane. The GFP-annexin V fusion proteins are used for the detection of apoptotic cells by flow cytometry or fluorescent microscopy. The fusion proteins provide for homogeneously labelled annexin, with fluorescence properties that do not change upon binding membrane of FITC-annexin V fluorescence by 40-50% occurs upon binding phospholipid
                                                                                                                       ABB57067 standard; protein; 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins are bifunctional Aequorea victoria green fluorescent protein (GFP) annexin fusion proteins, where the GFP and annexin moieties provide greater or equal fluorescent intensity and anionic phospholipid binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bifunctional fusion protein useful for the detection
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proteins are bifunctional Aequorea victoria green fluorescent prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 VDDLKSELTGKFEKLIVAMMKPSRLYDAYELKHALKGAGTDEKVLTEIIASRTPBELSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTBIIAGRTPEELRAI
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                                                                                                                                                                                                                           GDYKKALLLLC-GEDD 320
                                                                                                                                                                                                                                                               SIPAYLAETLYYAMKGAGTDDHTLIRVVVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
                                                                                                                                                                                                                                                                                         SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
                                                                                                                                                                                                                                                                                                                           KWGTDEEKFITIFGTRSVSHLRRVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                                                                                                                                                                                                                                                                                                                                                         KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                                                                                                                                                                                                                                                                                                                                                                                                                       KOVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL
                                                                                                                                                                                                      GDYKKALLLCGGEDD 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGTVTDFPGFDGRADAEVLRKAMKGLGTDEDSILNLLTSRSNAQRQEIAQEFKTLFGRDL
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                                                               (first entry)
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94.0%;
                           related protein sequence
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Pred. No. 1.2e
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occlusive
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ischaemia;
                             SEQ ID NO:136
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes (I) in a test sample or determining the expression profile of gene group in the sample comprising genes selected from (I). The met is useful for examining the ischaemic genes selected from (I). The met ischaemia, occlusive ischaemia or vasospastic ischaemia) by measurin expression levels of particular genes (ABI99202 to ABI9912, encodin profile sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression profile of a gene group comprising these genes are used as an indicator when screening for ischaemic condition improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent primers for a mouse ischaemic condition related sequence, which are in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Examining the ischemic condition (e.g. occlusive ischemia) by measur expression levels of particular genes defined in the specification of determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes.
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                                                                                                                                                                                                                                                                                 66 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKYLTEIIASRTPEELRAI
                                                                                                                                                                                                                                                                64 VDDLKSELTGKFEKLIVAMMKPSRLYDAYELKHALKGAGTDEKVLTEIIASRTPEELSAI
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                                                                                                                                                                                                                        KQVYBEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEI
                                                           SIPAYLAETLYYAMKGAGTDDHTLIRVVVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
                                                                                  SIPÄYLAETLYYAMKGÄGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
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GDYKKALLLLCGGEDD
                             GDYKKALLLLC-GEDD
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                                                                                                                                                                                            KQVYEEEYGSNLEDDVVGDTSGYYQRMLVVLLQANRDPDTAIDDAQVELDAQALFQAGEI
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Copyright (c) 1993 - 2004 Compugen Ltd
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                                                                                                                                                                                                                                    ANX5 HUMAN
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ANX6 MOUSE
ANX4 HUMAN
ANX4 PIG
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ANX4 CONPA
ANX8 CHICK
ANX8 RABIT
ANXB RABIT
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ANX7 HUMAN
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ANX2 BOVIN
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                                                                                P13928 homo sapien
P12429 homo sapien
O35639 mus musculu
P14669 rattus norv
P20073 homo sapien
Q07076 mus musculu
P79134 bos taurus
                                                                                                                                                                                                 P33477 oryctolagus
P50995 homo sapien
P97384 mus musculu
O35640 mus musculu
                                                                                                                                                                                                                                                                  P50994 canis famil
P51901 gallus gall
P55260 rattus norv
P27214 bos taurus
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P13214 bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                    3 rattus norv
3 gallus gall
5 cynops pyrr
4 mus musculu
                                                                                                                                                                                                                                                                                                                                                                   2 sus scrofa
7 rattus norv
3 homo sapien
                                hydra atten
homo sapien
xenopus lae
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                  bos taurus
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 rattus nor
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WZC_ECOL7
WZC_ECOL7
IF2_PSESM
DNL4_YEAST
CLPT_LACLA
MYH9_RAT
POLG_CXA24
ARSA_METJA
AWH3_HUMAN
                                                                                                                                                                                                                                                              ANX7 DICDI
ANX9 MOUSE
ANX4 FRANA
ANX1. GIALA
GIALA GIALA
GIAL GIALA
MYH9 CHICK
THS PYRAB
MYH9 FURAN
MYH9 FURAN
MYH9 FURAN
MYH9 FURAN
THS PYRAB
THSE PYRKO
THS DESY
MYH3 TAT
DVAL DICVI
YM67 YEAST
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ANX9 HUMAN
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ANXB XENLA
ANXD THOMAN
ANX2 CHICK
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Q9jhq0 mus mus P51074 fragari Q92108 gallus

076027

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mus mus columba

rattus sus scr

Q9nfs4 giardia P17063 giardia

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Q9v2q7 pyrococ Q52500 pyrococ

pyrococ pyrococ

730 thermoc 322 homo sa 346 desulfu

rattus

Q29471 canis f P51662 oryctol P14087 cavia c Q8hzm6 equus c Q8hzm6 esa P04083 homo sa P46193 bos tau

gallus xenopus xenopus homo sa

drosoph Bru sru

Q9vje5 P46338 P46338 Q8x719 P76387 Q87wq5 Q087387 Q06716 Q062812 P36290 P36290 Q58542

lactoco

9 escheric 7 escheric 5 pseudomc 7 saccharc

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african

P53379 sacchar

homo saj bos tau

P90970 caenorh Q03661 sacchar P08799 dictyos Q24702 dictyoc

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01-NOV-1988 (Rel. 09, 1
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Annexin A5 (Annexin V)
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Iwasaki A., Suda M., Nakao H., Nagoya
Iwasaki A., Sato F., Yoshizaki H., J
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P08758;
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                                                                                                                                                                                                                                            "Cloning and expression of cDNA for human phospholipid binding protein.", J. Biol. Chem. 263:8037-8043(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structure and expression of cDNA for an inhibitor of blood coagulation isolated from human placenta: a new lipocortin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=88163463; PubMed=2964863;
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Eur. J. Biochem. 174:585-592(1988).
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protein (PP4): homology with the lipocortin fami
Proc. Natl. Acad. Sci. U.S.A. 85:3708-3712(1988)
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Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
(CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
(Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
                                                                                                                                                                                                                                                                                                                   MEDLINE=88228020; PubMed=2967291; Kaplan R., Jaye M., Burgess W.H.,
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MEDLINE=95047484; PubMed=7958998;
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                                          nandez M.P., Morgan R.C
e gene encoding human a
h G+C content.";
e 149:253-260(1994).
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Chem. 263:10799-10811(1988)
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                                                                                               O., Fernandez M.R., Carcedo M.T.; annexin V has a TATA-less promoter with
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or human endonexin II, a Ca2+ a
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K.-S., Pratt D., Wachter
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Miyata
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RA Strausberg R.D., Collins F.S., Wagner L., Schaefer C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Blockins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length buman and mouse cDNA sequences."; "To marring Collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sedimentation equilibrium analysis of five lipocortin-related phospholipase A2 inhibitors from human placenta. Evidence against mechanistically relevant association between enzyme and inhibitor J. Biol. Chem. 263:18657-18663(1988).
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MEDLINE=92177413; PubMed=1311770;
Huber R., Berendes R., Burger A., Schneider
Luecke H., Roemisch J., Paques E.-P.;
                                                                                                                                                                                                                                         analysis
                                                                                                                                                                                                                                                                                                        MEDLINE=91085549; PubMed=2148156;
Huber R., Schneider M., Mayr I.,
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Huber R., Roemisch J., Paques E.-P.;
Huber R., Roemisch J., Paques E.-P.;
Withe crystal and molecular structure of human annexin V,
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                                                                                                                                                                                                       analysis at 2.0-A resolution. calcium channel activity.";
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-!- SUBUNIT: Monomer. Binds ATRX (By similarity).

-!- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.

-!- SIMILARITY: Belongs to the annexin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaneko N., Ago H., Matsuda R., Inagaki E., Miyano M.; "Crystal structure of annexin V with its ligand K-201 channel activity inhibitor.";
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J. Mol. Biol. 223:683-704(1992).
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MEDLINE=98118533; PubMed=9435213;
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-!- CAUTION: This protein has been independently sequenced by at least
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-!- FUNCTION: This protein is an anticoagulant protein that indirect inhibitor of the thromboplastin-specific comple is involved in the blood coagulation cascade.
-!- SUBUNIT: Monomer. Binds ATRX (By similarity).
-!- DOMAIN: A pair of annexin repeats may form one binding s calcium and phospholipid.
-!- SIMILARITY: Belongs to the annexin family.
-!- SIMILARITY: Contains 4 annexin repeats.
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10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
(CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
(CBP-I) (Pascular anticoagulant-alpha) (VAC-alpha)
                                                                                                                                                                                                                                                                                                                                                                                                                               Rodriguez-Garcia M.I., Morgan R.O.,
                                                                                                                                                                                                                                                                                                                                                            retrovirus."
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                                                                                                                                                                                                                                                                                                                                                                                                                    Fernandez M.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99072820;
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MEDLINE=96422179; PubMed=8824796;
Rodriguez-Garcia M.I., Kozak C.A., Morgan R.O.,
"Mouse annexin V chromosomal localization, cDNA
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Mus musculus (Mouse).
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P48036;
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0; PubMed=9854034;
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Rodentia;
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to the EMBL/GenBank/DDBJ databases.
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Sciurognathi; Muridae; Murinae; Mus
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Best Local :
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P14668;
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Annexin A5 (/
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Annexin; Calcium/phospholipid-binding;
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SWISS-2DPAGE; P48036; MOUSE.
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                                                                                                                                                                                                                   KWGTDEEKFITIFGTRSVSHLRRVFDKYMTISGFQ1
(Rel. 14, Created)
(Rel. 36, Last sequence update)
(Rel. 43, Last annotation updat
(Annexin V) (Lipocortin V) (Endc
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update) (Endonexin

II)

(Calphobindin

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Pepinsky R.B.,
Miller G.T., B
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use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.intorsend an email to licenses.
                                                                                                                                                                           Ohsawa K., Imai Y., Ito D., Kohsaka S.;
"Molecular cloning and characterization of annexin V-binding proteins
"Molecular cloning and characterization of annexin V-binding proteins
with highly hydrophilic peptide structure.";

J. Neurochem. 67:89-97(1996).

-!- FUNCTION: This protein is an anticoagulant protein that acts as ar
indirect inhibitor of the thromboplastin-specific complex, which
is involved in the blood coagulation cascade.

-!- SUBUNIT: Monomer. Binds ATEX and DNMT1.

-!- DOMAIN: A pair of annexin repeats may form one binding site for
calcium and phospholipid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
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"Five distinct calcium and phospholipid binding proteins share
homology with lipocortin I.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campos B., Mo Y.D., Mealy T.R.; Li C.W., Swairjo M.A., Balch C., Head J.F., Retzinger G., Dedman J.R., Seaton B.A.; "Mutational and crystallographic analyses of interfacial residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Ca (2+) -bridging mechanism and phospholipid head group recognition the membrane-binding protein annexin V."; Nat. Struct. Biol. 2:968-974 (1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93369587; PubMed=8362244; Concha N.O., Head J.F., Kaetzel M.A., Dedman J.R., Seaton B.A.; "Rat annexin V crystal structure: Ca(2+)-induced conformational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96035863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Wistar
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(Anchorin CII).
                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Wistar; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 37:8004-8010(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annexin V suggest direct interactions with phospholipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 2-319:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Swairjo M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96069783;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Structure of rat annexin V
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                                                                                                                                                                                                                                                                                                                                                                                              INTERACTION WITH DNMT1.
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                                                                                                                                               SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                               SIMILARITY: Belongs to the annexin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ky R.B., Tizard R., Mattaliano R.J., Sinclair L.K., G.T., Browning J.L., Chow E.P., Burne C., Huang K.S., D., Wachter L., Hession C., Frey A.Z., Wallner B.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chem. 263:10799-10811(1988).
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a; Chordata;
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(Vascular anticoagulant-alpha) (VAC-alpha)
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Sciurognathi; Muridae; Murinae; Rattus
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(See http://www.isb-sib
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tent is in no
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                                              and
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                                                                                                  a collaboration
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Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
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1A8A;
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       Similarity
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13-JAN-99.
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ACETYLATION
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                       1A755A7C11FA11CE CRC64;
       .6e-88;
              DB 1;
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              318;
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                       MEDLINE=94215900; PubMed=8163186; Fernandez M.P., Fernandez M.R., M
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EMBO J.
                                                                                                                                                                                                                  MEDLINE=90243721; PubMed=2159478; Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Deutzmann R., Mollender J., von der Mark K.; "The structure of anchorin CII, a collagen binding from chondrocyte membrane."; J. Biol. Chem. 265:8344-8344(1990).
                                                               SEQUENCE FROM N.
STRAIN=White leg
                                                                                                                                    Pfaeffle M., Ruggiero F., Yamada Y., Garrone R., vo
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90020458; PubMed=2552626; Moss S.E., Crumpton M.J.; "Alternative splicing or cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANXA5 OR ANX5.
Gallus gallus (Chicken).
Gukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauría; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Cal (CBP-I) (Placental anticoagulant protein I) (PAP-I) (Pracental anticoagulant anticoagulant-alpha)
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P17153;
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         of the
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n der Mark K.;
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                                                                                                                                                          Fernandez M.P.,
     (chick annexin V).";
                                                                                                                                                                                                                                                       protein isolated
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Pfam; PF00191; annexin; 4.
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"Structure of chicken annexin V at 2.25-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93249384; PubMed=8484740;
Boustead C.M., Brown R., Walker J.H.;
"Isolation, characterization and localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Contains 4 annexin repeats.
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U01673; AAB39917.1;
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U01671; AAB39917.1;
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291:601-608(1993).
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Amphibia; Batrachia; Caudata;
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            EMBL; D64134; BAA11012.1;
HSSP; P08758; 1AVH.
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                                                                         use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                             ifferential expression of annexin V during spermatogenesis in the freential expression of annexin V during spermatogenesis in the Cynops pyrrhogaster.";

Genes Evol. 206:64-71(1996).

FUNCTION: Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis (By similarity).

DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.

SIMILARITY: Belongs to the annexin family.

SIMILARITY: Contains 4 annexin repeats.
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                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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SMART; SM00335; ANX; 4.
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Annexin; Calcium/phospholipid-binding;
REPEAT 26 86 ANNEXIN 1
REPEAT 98 158 ANNEXIN 2
                                                                                                                                                                                                                                                                             MOUSE
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01-Apr.1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Prol
(Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II)
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Rodentia;
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                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                        ANX4 HUMAN STANDARD; PRT; 318 AA.

P09525; Q96F33; Q9BWXL;
01-MAR-1989 (Rel. 10, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I)
(Protein II) (P32.5) (Placental anticoagulant protein (PP4-X) (35-beta calcimedin) (Carbohydrate-binding pro
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                         HUMAN
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                             Homo sapiens (Human).
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or send a
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MGD; MGI:88255; Anxa6.
InterPro; IPR001464; Annexin.
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Pred. No. 7.7e
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
ANNEXIN 5.
ANNEXIN 6.
ANNEXIN 7.
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derye J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                         Ahn N.G.,
                                human placental annexin IV.";
J. Mol. Biol. 216:219-221(1990)
                                                                                                                                                              "Placental anticoagulant proteins: isolation and comparative characterization four members of the lipocortin family.";
                                                                                                                                                                                                                  SEQUENCE OF 1-14; 27-71; 99-143 AND 280-318. MEDLINE=89118212; PubMed=2975506; Tait J.F., Sakata M., McMullen R.A. Mian C
                                                                                                                                                                                                                                                                               phospholipase A2 inhibitors from human placer
mechanistically relevant association between
J. Biol. Chem. 263:18657-18663(1988).
                                                      "Crystallization and preliminary X-ray
                                                                                                    MEDLINE=91073383;
                                                                                                               X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                           ue nau. ..,
"Sedimentation equilibrium analysis of five lipocortin-related
"Sedimentation equilibrium of five lipocortin-related
phospholipase A2 inhibitors from human placenta. Evidence against a
phospholipase A2 inhibitors from between enzyme and inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 26-55; 98-123 AND 279-307. MEDLINE=89066652; PubMed=2974032;
                                                                                     Freemont
                                                                                                                                                                                               Tait J.F., Sakata M., McMullen
Hendrickson L.E., Fujikawa K.;
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MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Magner L., Shenmen C.M., Sc.,
Wagner L., Shenmen C.M., Sc.,
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Disteche C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Isolation and expression of cDNA coding for a new phospholipase A2 inhibitor family."; Behring Inst. Mitt. 82:59-67(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Chromosomal mapping of the human annexin IV (ANX4) gene.";
Genomics 12:313-318(1992).
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                                                                                                                                                  27:6268-6276(1988).
   Calcium/phospholipid-binding fusion and is involved in exoc
                                                                                83; PubMed=2254922;
Driessen H.P.C., Verbi
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a E., Kojima K.,
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REPEAT
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INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P13214; 1ANN.
SWISS-2DPAGE; P09525; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00196; ANNEXIN.
PRODOM; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PMMA-2DPAGE; P09525; -. Genew; HGNC:542; ANXA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00191; annexin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 106491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A42077; A42077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
              ANX4_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt DOMAIN:}\ A\ {\tt pair}\ {\tt of}\ {\tt annexin}\ {\tt repeats}\ {\tt may}\ {\tt form}\ {\tt one}\ {\tt binding}\ {\tt site}\ {\tt calcium}\ {\tt and}\ {\tt phospholipid.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M19383; AAC41689.1; ALT_INIT.
M82809; AAA51740.1; ...
D78152; BAA11227.1; ALT_INIT.
BC000182; AAH00182.1; ALT_INIT.
BC011659; AAH11659.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                               184;
                                                                                                                                                                                                                                   187
                                                                                                                                                                                                                                                                                            127
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                                                                                                                                                                                                                                                                                                                                               DDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calcium/phospholipid-binding; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00223; ANNEXIN; 4.
                                                                                                                                                                                                                                                                                                                                                                                                               GTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLL
                                                                                                                                                                                                                                                                                         QVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELK 186
                                                                                                                                                                                                                                                                                                                                                                                   GTVKAASGFNAMEDAQTLRKAMKGLGTDEDAIISVLAYRNTAQRQEIRTAYKSTIGRDLI
                                                                                                                                                                   IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG
                                                                                                                                                                                                                                  WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
                                                                                        DYRKVLLVLCGGDD
                                                                                                                   DYKKALLLLCGEDD 320
                                                                                                                                              KSAYFAEKLYKSMKGLGTDDNTLIRVMVSRAEIDMLDIRAHFKRLYGKSLYSFIKGDTSG
                                                                                                                                                                                                        WGTDEVKFLTVLCSRNRNHLLHVFDEYKRISQKDIEQSIKSETSGSFEDALLAIVKCMRN
                                                                                                                                                                                                                                                                QTYQQQYGRSLEDDIRSDTSFMFQRVLVSLSAGGRDEGNYLDDALVRQDAQDLYEAGEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001464; Annexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
94
178
253
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                 STANDARD;
                                                                                                                                                                                                                                                                                                                          SGNFEQVIVGMMTPTVLYDVQELRRAMKGAGTDEGCLIEILASRTPEEIRRIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seems to bind one calcium ion with high affinity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35751 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.
                                                                                        318
                                                                                                                                                                                                                                                                                                                                                                                                                                               53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 933;
Pred. No. 1
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R -> Q (IN REF.
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                   PRT;
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                    318
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P08132; Q29306;

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01-AUG-1988 (Rel. 08, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin (Protein II) (P32.5) (Placental anticoagulant prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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MEDLINE=87275850; PubMed=2956093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for protein kinase C; the binding proteins."; EMBO J. 6:1599-1604(1987).
                                                                                                                                                                                                                   PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
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Mamm. Genome 7:509-517(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96327607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-126 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
                                                                                                                                                                                                                                                                PIR; A27107; LUPG4.
HSSP; P13214; IANN.
InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Winteroe A.K., Fredholm M., Davies W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The amino acid sequence of protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leber K.,
                                                                                                                                                                                                                                                                                                                        EMBL; F14682; CAA23194.1; -.
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                                                          SEQUENCE
                                                                                                                                                                                        Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;
                                                                                                                                                                                                       PROSITE; PS00223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSUE=Small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the annexin fami
SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
MISCELLANBOUS: Seems to bind one calcium ion with high affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Calcium/phospholipid-binding protein/which promotes membrane fusion and is involved in exocytosis (By similarity).
 185;
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnsson
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                                                          318 AA;
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    Conservative
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                 58.2%;
58.9%;
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domain structure Ca2+-modulated lipid
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                                                          ANNEXIN 1.

ANNEXIN 2.

ANNEXIN 3.

ANNEXIN 4.

ACETYLATION (PROBABLE).

PHOSPHORYLATION (BY PKC).

PA7D9CE2B7C631E8 CRC64;
    51;
                Score 931; DB 1;
Pred. No. 1.6e-53;
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    Mismatches
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PRINTS; PR00196; ANNEXIN.

PRODOM; PD000143; ANNEXIN; 8.

SMART; SM00335; ANX; 8.

PROSITE; PS00223; ANNEXIN; 7.

Annexin; Calcium/phospholipid-binding; Repeat.

INIT_MET 0 0 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996
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10-OCT-2003
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                                                                                                                                                                                                                                                                  HSSP; P79134; 1AVC.
InterPro; IPR001464; Annexin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fan H., Josic D., Lim Y.P., Reutter W.; "cDNA cloning and tissue-specific regulation of expression of calcium-binding protein 65/67. Identification as a homologue of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of
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P48037;
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10-OCT-2003 (Rel. 42, Last annotation update)
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)
(Chromobindin 20) (67 KDa Calelectrin) (Calphobindin-II) (CP3-II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Calcium-binding protein CATA 65/67).
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MISCELLANEOUS: Seems to bind one calcium i
SIMILARITY: Belongs to the annexin family.
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                                                                                                                                                                                                                                                                                                                                               S65683; S52844.
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Sciurognathi; Muridae; Murinae; Rattus.
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                                                    SEQUENCE FROM N.A., AND PAKTIAL CARRESTORY
MEDLINE=88124902; PubMed=2963335;
Suedhof T.C., Slaughter C.A., Leznicki I.,
"Human 67-kDa calelectrin contains a dupli
"Human in 35-kDa lipocortins.";
found in 35-kDa lipocortins.";
                                                                                                                                                                                                                                                                                                                             P08133;
01-AUG-1988 (Rel. 08, Created,
01-APR-1990 (Rel. 14, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Annexin A6 (Annexin VI) (Lipocortin VI) (P68)
Annexin - 24: - 20) (67 kDa calelectrin) (Calph
                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=88196081; PubMed=3258820;
MEDLINE=88196081; PubMed=3758820;
                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
MEDLINE=89380132; PubMed=2528541; Iwasaki A., Suda M., Watanabe M., Saino Y., Shidara Y., Maki M.;
                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                        SEQUENCE FROM N.A.
                                                                                                                                                                "Primary structure of the human, protein p68 a novel member of a pembo J. 7:21-27(1988).
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672 AA;
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Primates;
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Watanabe M., Maki M.;
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Pred. No. 4
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               Nakao
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            Ή.,
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                                                                                                          Barjon
           Hattori Y.,
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           Nagoya
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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Brownstein M.J., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B., Wadin T.B.
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                                                                                                                                                                                                                                                                                                                              EMBL; D00510; BAA00400.1; -.
EMBL; Y00097; CAA68286.1; -.
EMBL; J03578; AAA35656.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The structure of recombinant human annexin VI in crystals membrane-bound.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96326697; PubMed=8709
Benz J., Bergner A., Hofmann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yoshizaki H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the annexin fami
-!- SIMILARITY: Contains 8 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- MISCELLANEOUS: Seems to bind one calcium ion
-!- SIMILARITY: Belongs to the annexin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huber R., Voges D.;
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                                                                    Pfam; PF00191; annexin; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    otein from human placenta.";
Biochem. 107:43-50(1990).
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1M91; 15-APR-03
                                                                                                                                                   114070;
                                                                                                                                                                                                                                                                                                BC017046; AAH17046.1;
                                                                                                                                                                              HGNC:544; ANXA6.
   PR00196; ANNEXIN. PD000143; Annexin; 8
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Annexin; Calcium/phospholipid-binding; Repeat; Acetylation; Phosphorylation; 3D-structure.
INIT_MET 0 0
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                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANX 4 MOUSE
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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S -> T (IN REF. 2).
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Pred. No. 7.2e-53;
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Sciurognathi; Muridae;
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DOMAIN: A pair of annexin repeats calcium and phospholipid.

MISCELLANEOUS:

Belongs to

the bind

annexin family.

one calcium

with high affinity

may form one

binding

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ANX4 BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY BO ID ANY B
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Best Local S
Matches 181
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01-JAN-1990
10-OCT-2003
Mammalia; Eutheria; Cetartiodactyla;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                   ANX4_BO
                                                                                                                                                                                                                                                                                                                           BOVIN
                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata;
                                                                                                                                            01-JAN-1990 (Rel. 13, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromcbindin (Protein II) (P32.5) (Placental anticoagulant protein II) (PAP-II) (PP4-X) (35-beta calcimedin) (Carbohydrate-binding protein P33/P41)
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HSSP; P13214;
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PD000143; Annexin
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DYRKVLLILCGGDD 318
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(Rel. 13,
(Rel. 42,
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
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BY SIMILARITY.
                                                               Craniata; Vertebrata; Euteleostomi
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                                          Ruminantia; Pecora; Bovcidea
                                                                                                                                                                                                                                                                                                        318
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EMBL; M22248; AAA30507.1; -.
EMBL; X13627; CAA31954.1; -.
EMBL; D78178; BAA11243.1; -.
PIR; A31578; LUBO4.
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                                                                                                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- DOMAIN: A pair of annexin repeats may f
calcium and phospholipid.
-!- MISCELLANEOUS: Seems to bind one calciu
-!- SIMILARITY: Belongs to the annexin fami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structure of the trigonal crystal form of bovine annexin IV.";
Biochem. J. 329:101-106(1998).
-!- SUBUNIT: Monomer.
-!- DOMAIN: A pair of annexin repeats may form one binding site
                                                                                                                  HELIX
                                                                                                                                                                                                                                                                Annexin;
                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kojima K., Yamamoto K., Irimura T., Osawa T., Ogawa H., Ma
"Characterization of carbohydrate-binding protein p33/41:
"ith annexin IV, molecular basis of the doublet forms (p3)
and modulation of the carbohydrate binding activity by
                                                                                                                                                                                                                                                 INIT MET
                                                                                                                                                                                                                                                                                                             ProDom;
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                                                                                                                                                                                                                                                                                                                                              Pfam; PF00191; annexin;
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MEDLINE=96205957; PubMed=8631806;
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"Cloning and characterization of a cDNA
(chromobindin 4).";
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TISSUE=Liver;
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                                                                                                                                                                                                                                                           Calcium/phospholipid-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biophys. Res. Commun. 156:660-667(1988).
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O1-OCT-1996 (Rel. 34, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Annexin A4 (Annexin IV) (Lipocortin IV) (36 k
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ANXA4 OR ANX4.
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                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog).
                                                                                          SEQUENCE OF 1-9
                                                                                                                              Fukuoka S.-I., Horst K., Kazuki-Sugino R., Ikeda Y.; "Cloning and characterization of ZAP36, an annexin-like, z granule membrane associated protein, in exocrine pancreas. Biochim. Biophys. Acta 1575:148-152(2002).
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                       Mammalia;
                    Fukuoka S.-I.;
"Analysis of ZAPs,
                                                                   MEDLINE=94362286;
  regulated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WGTDEVKFLTVLCSRNRNHLLHVFDEYKRIAQKDIEQSIKSETSGSFEDALLAIVKCMRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTYQLQYGRSLEDDIRSDTSFMFQRVLVSLSAGGRDESNYLDDALMRQDAQDLYEAGEKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYKKALLLLCGEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSAYFAERLYKSMKGLGTDDDTLIRVMVSRAEIDMLDIRANFKRLYGKSLYSFIKGDTSG
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                                                                                                                                                                                                                                                                                                                                     Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
    exocytosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                   PubMed=7765250
                                                                                                                                                                                                                                                                      AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.8%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                         Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320
    en granule membrane of the pancreas.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 924; DB 1;
Pred. No. 4.6e-53;
                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; ; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86BDBDF349D774FD CRC64;
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                                                                                                                                                                                                                                                                        78-95
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                           associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    zymogen
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Canis.
                             proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    granule
                                                                                                                                                                                    zymogen
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                                 r:
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Matches 180;

Conservative

54

80;

Indels

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9 67 σ 7

DDLKSELSGNFERVIVGMITPTVLYDVQELRRAMKGSGTDEGCLIEILASRTPEELRC DDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA GTVKPASGFSATEDAQTLRKAMKGLGTDEDAIISVLAPRNTSQRQEIRTÄYKSTIGRD GTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRD

QVYBEBYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVBQDAQALFQAGE

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QTYQLQYGRSLEDVIRSDTSFMFQRVLVSLSAGGRDEGNFLDDALMRQDAQDLYEAGE

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187 125 127

185

WGTDEVKFLTVLCSRNRNHLLHVFDEYKRISQKDIEQGIKSETSGSFEDALLAIVKCM

WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSI

KSAYFAERLYKSMKGLGTDDNTUIRVMVSRAEIDMMDIRESFKRLYGKSLYSFIKGDT IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDT

ANX6 AC DT DT DT DT DE

P51901; 01-OCT-1996 01-OCT-1996 10-OCT-2003

(Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 42, Last snnotation update)
(Annexin VI) (Lipocortin VI) (198)

(67 kDa calelectrin) (Calphobindin-II)

(P70)

(Protein III) 1-II) (CPB-II)

Annexin A6 (Annexin (Chromobindin

맑 S 밁 Š 문

305

DYRKVLLILCGGDD DYKKALLLLCGEDD

318 320 245

247

307

RESULT

CHICK

ANX6

CHICK

STANDARD;

671

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Query Match
                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaborative in the Swiss Institute of Bioinformatics and the EMBL outsets the European Bioinformatics Institute. There are no restrictions of use by non-profit institutions as long as its content is in memodified and this statement is not removed. Usage by and for commentities requires a license agreement (See http://www.isb-sib.ch/ann
                                                           REPEAT
REPEAT
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biosci. Biotechnol. Biochem. 58:1282-1285(1994)
                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                  -!- MISCELLANEOUS: Seems to bind one calcium ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     +
                                                SEQUENCE
                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                    InterPro; IPR001464;
                                                                                                                                                                                                                                  HSSP; P13214; 1ANN
                                                                                                                                                                SMART; SM00335; ANX; 4.
                                                                                                                                                                                                        Pfam; PF00191; annexin;
                                                                                                                          INIT MET
                                                                                                                                                                              ProDom; PD000143; Annexin; 4.
           Local
                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis (By similarity) DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the annexin fami
SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                       (By similarity)
                                                                                                                                                                                                                                               D38223; BAA07398.1; -.
           Similarity
                                                                                                                                                                                             PR00196; ANNEXIN.
                                                                                                                                         PS00223; ANNEXIN; 4. Calcium/phospholipid-binding;
                                               22
94
178
253
138
318
                                                  AΑ;
                                                             138
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154
238
313
                                                    35681
           56.9%;
                                                                                                                                                                                                                      Annexin.
                                                    MW.
Score 911; DB
Pred. No. 3.2e
54; Mismatches
                                                                ANNEXIN 1.
ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
V -> D (IN
                                                                                                                                                                                                                                                                                                                                                                                             annexin family.
                                                    42EF5B89179B4863
                                                                 D (IN REF.
              DB 1;
.2e-52;
                                                      AA SEQUENCE)
CRC64;
                           Length
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Best Local S
Matches 185
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SEQUENCE
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; S67466; AAB29337.2; -. PIR; JC2029; JC2029. HSSP; P79134; IAVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00191; annexin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         calcium and phospholipid.
-!- SIMILARITY: Belongs to the annexin family.
-!- SIMILARITY: Contains 8 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 197:556-561(1993).

-I- FUNCTION: May associate with CD21. May regulate the release Ca(2+) from intracellular stores (By similarity).

-I- DOMAIN: A pair of annexin repeats may form one binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94092130; PubMed=8267590;
Cao X., Genge B.R., Wu L.N., Buzzi W.R., Showman
"Characterization, cloning and expression of the
"Chicken growth plate cartilage matrix vesicles.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00196; ANNEXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001464; Annexin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANXA6 OR ANX6.
     303
                                                                                                  243
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                                                                                                                                                                                                    183
                                                                                                                                                                                                                                                   126
                                                                                                                                                                                                                                                                                  123 RAIKQVYEBEYGSSLEDDVYGDTSGYYQRMLYVJLQANRDPDAGIDEAQVEQDAQALFQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185;
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                                                                                                                                                                                                                                                                                                                                                                                    63 RDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEEL
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                                                                                SIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKG
                                                                                                                                                                                                                                       HDLVAAYKDAYERDLEADVVGDTSGHFKKMLVVLLQGAREEDDVVSEDLVEQDAKDLLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFG
DTSGDYKKALLLLC-GEDD
                                        CVRSTAEYFAERLYKAMKGLGTRONTLIHIMVSRSEIDMLDIREVFRTKYDKSLHNMIKE
                                                                                                                                       GELKWGTDEAQFIYILGRRSKQHLRMVFDEYLKISGKPIERSIRAELSGDFEKLKLAVVK
                                                                                                                                                                        GELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVK
                                                                                                                                                                                                                                                                                                                                      KDLIADLKYELTGKFERLIVSLMRÞPAYSDÁKEIKDÁIAGIGTDEKCLIEILÁSRTNQEI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                        KVYRGSVKDFPGFNASQDADALCNAMKGFGSDKDAILDLITSRSNKQRLEICQAYKSQYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calcium/phospholipid-binding; Repeat.
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99
183
258
370
442
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607
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502
592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 904.5;
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ANNEXIN 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 2.1e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wuthier R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               671;
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                                                                                                                                                             Matches 178;
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                              REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and cuarecurry granule membrane associated protein, in exocrine pancreas.";

granule membrane associated protein, in exocrine pancreas.";

Biochim. Biophys. Acta 1575:148-152(2002).

-!- FUNCTION: Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TANX4 RAT
P55260;
01-OCT-1996
                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstations the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                              SMART; SM00335; ANX; 4.
                                                                                                                                                                                                                                                                                                                                            ProDom; PD000143; Annexin; 4.
                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00196; ANNEXIN.
                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D38224;
HSSP; P13214;
                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the annexin family.
-!- SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- MISCELLANEOUS: Seems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- DOMAIN: A pair of annexin repeats may form
calcium and phospholipid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fukuoka S.-I., Horst K., Kazuki-Sugino F "Cloning and characterization of ZAP36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Wistar; TISSUE=Pancreas; MEDLINE=22015264; PubMed=12020832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Annexin A4 (Annexin IV) (Lipocortin IV) (36 kDa zymogen granule membrane associated protein) (ZAP36).
ANXA4 OR ANX4. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation updat
                                                                                                                                                                                                                                                                                        INIT MET
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                                                                                                                                                                           Local
                    127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (By similarity).
                                               65
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                                                                                                                                                                        Similarity
QVYEEBYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELK
                                                                                                                                                                                                                                                                                   EDLKSELSSNFEQVILGMMTPTVLYDVQELRRAMKGAGTDEGCLIEILASRNPEEIRRIN
                                                                   DDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 126
                                                                                                 GTVKAASGFNATEDAQVLRKAMKGLGTDEDAIIGVLACRNTAQRQEIRTAYKSTIGRDLL
                                                                                                              GTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLL
                                                                                                                                                                                                                  253
318 AA;
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22
94
178
                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                82
154
238
313
                                                                                                                                                                                                                  35717 MW;
                                                                                                                                                                        56.4%;
56.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to bind one calcium ion
                                                                                                                                                           54;
                                                                                                                                                       Score 903; DB 1;
Pred. No. 1.1e-51
4; Mismatches 8
                                                                                                                                                                                                                                          ANNEXIN 1.
ANNEXIN 2.
ANNEXIN 3.
                                                                                                                                                                                                                                ANNEXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                FF630ABEA22ED2E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R., Ikeda Y.;
an annexin-like, zymogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą
                                                                                                                                                          82;
                                                                                                                                                                                  Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with high affinity
                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a collaboration
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                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P27214; P27215;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Annexin All (Annexin XI) (Calcyclin-associated annexin 50) (CAP-50)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANXB
                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                             use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                               "Alternatively spliced annexin XI transcripts differ near the amino-terminus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92305067; PubMed=1535225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Chondrocytes; MEDLINE=92184796; PubMed=1372001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANXA11 OR ANX11
GO; GO:0005635; C:nuclear membrane; ISS GO; GO:0005654; C:nucleoplasm; ISS GO; GO:0005515; F:protein binding; ISS.
                                                        PIR; A42113; LUBO11.
PIR; S23447; S23447.
                                                                                                                                                                                                                                                                                        Name=2;
IsoId=P27214-2; Sequence=VSP_000289;
IsoId=P27214-2; Sequence=VSP_000289;
-!- TISSUE SPECIFICITY: Expressed in a wide variety of tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Towle C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                            HSSP; P13214;
                                                                                     EMBL; M82802; AAA30379.1; -.
EMBL; Z11742; CAA77801.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of a novel mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol.
                                                                                                                                                                                                                                                 calcium and phospholipid.
SIMILARITY: Belongs to the annexin family.
SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                       Name=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.A., Weissbach
                                                                                                                                                                                                                                                                                                                                                       IsoId=P27214-1; Sequence=Displayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A., Treadwell B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and ubiquitous expression of the annexin Chem. 267:5416-5423(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPAYFAERLYKSMKGLGTDDSTLIRVMVSRAEIDMLDIPANFKRVYGKSLYSFIKGDTSG
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                                              1AOW.
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                                                                                                                                                                          institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                   splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             L., Treadwell B.V.;
                                                                                                                                                                                                                                                                                                                                                                                      Named isoforms=2;
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                                                                                                                                                                                        There are no restrictions
                                                                                                                                               http://www.isb-sib
                                                                                                                                                           Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                 encode proteins
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XI gene.
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Oryctolagus cuniculus (Rabbit)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolag

Oryctolagus

Euteleostomi;

TISSUE=Lung;

SEQUENCE FROM N.A., NCBI_TaxID=9986;

AND PARTIAL

SEQUENCE

MEDLINE=92378579; PubMed=1380798;

Okumitsu H., Mizutani

Molecular cloning of rabbit CAP-50, a calcyclin-associated

A., Muramatsu

M.-A., Yokota

H :

Arai K.-I.,

annexin

-!- DOMAIN:

A pair of

annexin repeats may form

binding

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annexin family.

calcium and SIMILARITY:

Biochem. protein.",

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186:1227-1235(1992)

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ANXB
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Best Local S
Matches 174
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                                                                                                                                                                                                                                 ANXB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Pfam; PF00191; annexin; 4.
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28-FEB-2003
                                                                                                                                                                        ANXALL OR ANXLL
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                                                                                                                                                                                                              01-FEB-1994
                                                                                                                                                                                                                       P33477;
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                                                                                                                                                                                                                                                                                                                       NTPAFFAERLNKAMRGAGTKDRTLIRIMVSRSEIDLLDIRAEYKRLYGKSLYHDITGDI
                                                                                                                                                                                                                                                                                                                                         SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGD
                                                                                                                                                                                                                                                                                                                                                            RLGTDESKFNAILCSRSRAHLVAVFNEYQRMTGRDIEKSICREMSGDLEQGMLAVVKCI
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                                                                                                                                                                                                                                                                                                                                                                                                                   KOVYEEEYGSSLEDDVVGDTSGYYORMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGE
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                                                                                                                                                                     (Rel. 28, Createw, (Rel. 28, Last sequence update, (Rel. 41, Last annotation update)
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279
363
438
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NO. 1.2e-49;
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                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3AF6503CCA6D05A1 CRC64;
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01-OCT-1996
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NCBI_TaxID=9606;
                                                               Mammalia; Eutheria; Primates;
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(Rel. 42, Last annotation update)
(Annexin XI) (Calcyclin-associate
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ANNEXIN 3.
                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Schzelton M.J., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Schzetz T.E., Ra Brownstein M.J., Ugdin T.B., Toshiyuki S., Carrinici P., Prange C., RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carrinici P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., WcEwan R.Y., Malek J.A., Gunaratne P.H., RA Robards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., VAN PARLES, Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Ra Minting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Ra Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schmutz J., Schmutz J., Myers R.M., Schmutz J., Schmutz J., Myers R.M., Schmutz J., Schmutz J., Myers R.M., Schmutz J., Schmutz J., My
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EMBL; BC007564; AAH07:
PIR; A53152; A53152.
HSSP; P13214; 1AOW.
                 GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005635; C:nuclear membrane; NAS.
GO; GO:0005634; C:nucleoplasm; NAS.
GO; GO:0005643; F:phospholipid binding;
GO; GO:0005543; F:protein binding; IPI.
GO; GO:0005515; F:immune response; TAS.
InterPro; IPR001464; Annexin.
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MEDLINE=94140847; PubMed=7508441;

Misaki Y., Pruijn G.J.M., van der Kemp

"The 56K autoantigen is identical to hu

J. Biol. Chem. 269:4240-4246(1994).
                                                                                                                                                                                                                 Genew; HGNC:535; ANXA11.
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MEDLINE=22388257; PubMed-..
R.L., Feingold
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Bances P., Fernandez M.R., Rodriguez-Garcia M.I., Morgan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            calcium and phospholipid.

DISEASE: Antibodies against ANXAll are present in sera patients with various autoimmune diseases, predominantly from patients with rheumatoid arthritis, systemic lupus erythematosus, or Sjogren's syndrome.

SIMILARITY: Belongs to the annexin family.

SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                             602572;
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Feingold E.A., Gr
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  (See http://www.isb-sib.ch/announce/
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01-NOV-1997
                                                                                                                                                                                                                                         MEDLINE=97092887; PubMed=8938449;
Fernandez M.P., Jenkins N.A., Gil
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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      Genomics
                                                                 Bances P., Fernandez Fernandez M.P.;
                                                                                                                                                                                    "Sequence and chromosomal localization Genomics 37:366-374(1996).
                                                                                                                                                                                                                       Morgan R.O.;
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                      WEDLINE=20469408; PubMed=11013079;
                                           Annexin All
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; PD000143; Annexin;
SM00335; ANX; 4.
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                      All (ANXAll) gene structure as the progenitor of and source of orthologous cDNA isoforms.";
        69:95-103 (2000).
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(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
(Annexin XI) (Calcyclin-associated
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/FTId=VAR 012006.

I -> V (in dbsNP:1802932).

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W; 4ADCAC8F270BFEE4 CRC64;
                                                                                    Rodriguez-Garcia M.I.,
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Pred. No. 5.3e-49;
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Best Local Sim
Matches 170;
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EMBL; AJZ89763; CAB94770.1; J
EMBL; AJZ89764; CAB94770.1; J
EMBL; AJZ89765; CAB94770.1; J
EMBL; AJZ89766; CAB94770.1; J
EMBL; AJZ89766; CAB94770.1; J
EMBL; AJZ89767; CAB94770.1; J
EMBL; AJZ89769; CAB94770.1; J
EMBL; AJZ89769; CAB94770.1; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collabo between the Swiss Institute of Bioinformatics and the EMBL outstathe European Bioinformatics Institute. There are no restrictions of the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         calcium and phospholipid.
-!- SIMILARITY: Belongs to the annexin fami
-!- SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage _{\parallel} by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- DOMAIN: A pair of annexin repeats may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION:
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00191; annexin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005635; C:nuclear membrane; ISS GO; GO:0005654; C:nucleoplasm; ISS. GO; GO:0005515; F:protein binding; ISS. InterPro; IPR001464; Annexin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P13214; 1ANN.
SWISS-2DPAGE; P97384; MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L; AJZ89760; CAB94770.1; JOINED.
L; AJZ89761; CAB94770.1; JOINED.
L; AJZ89763; CAB94770.1; JOINED.
L; AJZ89763; CAB94770.1; JOINED.
L; AJZ89764; CAB94770.1; JOINED.
L; AJZ89765; CAB94770.1; JOINED.
L; AJZ89766; CAB94770.1; JOINED.
L; AJZ89768; CAB94770.1; JOINED.
L; AJZ89769; CAB94770.1; JOINED.
L; AJZ89769; CAB94770.1; JOINED.
L; AJZ89769; CAB94770.1; JOINED.
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                                                        369
                                                                                                              309
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  429
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                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                           Calcium/phospholipid-binding;
207 267 ANNEXIN 1
                                                                                                                                                                                                                         RGTITAASGFDPLRDAEVLRKAMKGFGTDEQAIIDCLGSRSNKQRQQILLSFKTAYGK
                                                                                                                                                                  LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTBIIASRTPEELR
                                                                                                                                                                                                                                                 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGR
                          SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGI
                                                       SRAYKTEFOKTLEEAIRSDTSGHFORLLISLSOGNRDESTNVDMSLVQRDVQELYAAG
                                                                                                                                      KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAG
                                                                         KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKS
  NTPAFFAERLNKAMRGAGTKDRTLIRIMVSRSELDLLDIRAEYKRMYGKSLYHDITGI
                                                                                                                                                                                                                                                                                                                                      503
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                    438
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                                                                                                                                                                                                                                                                                                                                                                                                                          ANNEXIN; 4.
                                                                                                                                                                                                                                                                                                                                                      498
                                                                                                                                                                                                                                                                                                                                                                   339
423
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                                                                                                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                                                                 Score 857; DB
Pred. No. 1.7e-
59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   ANNEXIN
                                                                                                                                                                                                                                                                                                                                                      ANNEXIN
                                                                                                                                                                                                                                                                                                                                         424B1345E0F4EC8A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                             Repeat.
                                                                                                                                                                                                                                                                                                              DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1201374; Anxa8.
InterPro; IPR001464; Annexin
Pfam; PF00191; annexin; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00196; ANNEXIN. ProDom; PD000143; Annexin; 4.
                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                 Annexin;
                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ002390; CAA05364.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Fetal;
MEDLINE=98096578; PubMed=94349
                                                                                                                                                                                                                                                                                                                                                         SMART; SM00335; ANX; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The genetic origin of mouse annexin VIII.";
Mamm. Genome 9:8-14(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fernandez M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              035640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morgan R.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANXA8 OR ANX8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Annexin A8 (Annexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANX8 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: This protein is an anticoagulant protein that acts as a indirect inhibitor of the thromboplastin-specific complex, which is involved in the blood coagulation cascade (By similarity). DOWAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.

SIMILARITY: Belongs to the annexin family.

SIMILARITY: Contains 4 annexin repeats.
                                187
                                                       134
                                                                                  128
                                                                                                          74
                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                     P14668; 1A8B.
                                                                                                                                                             14
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                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an email to license@isb-sib.ch).
                                                   AYEEDYGSTLEEDIQGDTSGYLERILVCLLQGSRDDVSGFVDPGLVLQDAQALHEAGEKI
                                                                                                   TLKSELSGKFERLIVALMYPPYSYEAKELHDAMKGLGTKEGVIIEILASRTKNQLREIMK
                                                                                                                                                                                                                                                                                                                   Calcium/phospholipid-binding; Repeat; 38 90 ANNEXIN 1.
MGTDEMKFİTİLCTRSLTHLMRVFEEYEKIADKCIEDSFKSETHGSLEEAMLTVVKCTRN
                       WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
                                                                          VYBEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAG-IDEAQVEQDAQALFQAGELK 186
                                                                                                                      DLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQ
                                                                                                                                                     TVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLD
                                                                                                                                                                                                                                                                                                                                             PS00223; ANNEXIN; 4
                                                                                                                                                                                                                                                                 270
327 AA;
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                          110
195
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(Rel. 40,
(Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copeland N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in VIII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=9434938;
opeland N.G., Gilbert D.J.,
                                                                                                                                                                                                                                                                                162
247
322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                 36843 MW;
                                                                                                                                                                                                                          52.7%;
57.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last
                                                                                                                                                                                                              49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence update)
                                                                                                                                                                                                                                                                            ANNEXIN 1.
ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
                                                                                                                                                                                                                        Score 842.5; DB Pred. No. 9e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                              2CC6163642D29EA0 CRC64;
                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327
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                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                             84;
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                                                                                                                                                                                                                                                                                                                            Blood coagulation
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                    327;
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                                                                                                                                                                                                          Gaps
                          246
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 253
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschenko L., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Toschman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E.,
RA Schen J.E.,
RA Schen J.E.,
RA Schen J.E.,
RA Schen J.S., Sanchez J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16993(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
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01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Annexin A8 (Annexin VIII) (Vascular anticoagulant-beta) (VAC-beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Placenta;
TISSUE=Placenta;
MEDLINE=90032687; PubMed=2530088;
Maurer-Fogy I., Krystek E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chang K.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92216091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein that inhibits coagulation and phospholipase A2 activit molecular cloning, expression and comparison with VAC-alpha.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leukemia."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trujillo J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                    FUNCTION: This protein is an anticoagulant protein indirect inhibitor of the thromboplastin-specific is involved in the blood coagulation cascade. DOWAIN: A pair of annexin repeats may form one bir calcium and phospholipid.

SIMILARITY: Belongs to the annexin family.
               SIMILARITY: Belongs to the annexin fami SIMILARITY: Contains 4 annexin repeats.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. 185:63-71(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YYKTALLNLVGTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2216091; PubMed=13137714;
., Wang G., Freireich E.J.,
J.M., Stass S.A.;
expression of the annexin V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   руккацьцссер 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feingold E.A., Grouse L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Primates;
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Catarrhini;
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                                                                                                     binding site
                                                                                                                                                                      complex,
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Best Local Sin
Matches 177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC004376; AAH04376.1; -.
EMBL; A07358; CAA00657.1; -.
PIR; S06476; LUHU8.
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EMBL; M81844; AAB46383.1; -.
-ANX3 HUMAN
P12429;
01-OCT-1989
01-OCT-1989
10-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Placenta;
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                                                      HUMAN
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                                                                                                                                                                                                                                                                                                                                                                  Similarity_ 56.
77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Calcium/phospholipid-binding; Repeat;
                                                                                                                                                                                                                                AYEEDYGSSLEEDIQADTSGYLERILVCLLQGSRDDVSSFVDPALALQDAQDLYAAGEKI
                                                                                                                                                                                                                                                   VYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDP-DAGIDEAQVEQDAQALFQAGELK 186
                                                                                                                                                                                                                                                                           TLKSELSGKFERLIVALMYÞÞYRYBAKELHDAMKGLGTKEGVIIBILASRTKNQLRBIMK 133
                                                                                                                                                                                                                                                                                               DLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQ
                                                                                                                                                                                                                                                                                                                     TVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLD
                                                                                                                                                                                     WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
                                                                                                                                          LHSYFAERLYYAMKGAGTRDGTLIRNIVSRSEIDLNLIKCHFKKMYGKTLSSMIMEDTSG
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                                                                                                  DYKNALLSLVGSD
                                                                                                                     руккацциссер
                                                                                                                                                          IPAYLAETLYYAMKGAGTDDHTLIRVMYSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG
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313
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262
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(Rel. 12,
(Rel. 42,
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ANNEXIN 3.
ANNEXIN 3.
ANNEXIN 4.
A -> S.
/FTId=VJR 000604.
Q -> T (IN REF. 2).
F -> L (IN REF. 2).
R -> G (IN REF. 2 AND 3).
A -> G (IN REF. 2 AND 3).
GD -> RY (IN REF. 2)
  sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                            Score 832.5;
Pred. No. 4e-
                                                                                                                                                                                                                                                                                                                                                                                                              ) -> RY (IN REF. 2
3AAEE1D7072A9379
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X-RAY CRYSTALLOGRAPHY MEDLINE=96229894; PubM

Lewit-Bentley A., Russo-Marie

NPHY (1.8 ANGSTROMS) PubMed=8639653;

Biochemistry characterization

27:6268-6276(1988).

the

lipocortin

family.";

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RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Basak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RI proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pepinsky R.B., Tizard R., Mattaliano R.J., Sinclair L.K., Miller G.T., Browning J.L., Chow E.P., Burne C., Huang K.-S., Pratt D., Wachter L., Hession C., Frey A.Z., Wallner B.P.; "Five distinct calcium and phospholipid binding proteins share homology with lipocortin I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Annexin A3 (Annexin III) (Lip
protein III) (PAP-III) (35-al
phosphate 2-phosphohydrolase)
ANXA3 OR ANX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=88273202; PubMed=2968983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94102764; PubMed=8276419; Tait J.F., Smith C., Xu L., Cookson "Structure and polymorphisms of the Genomics 18:79-86(1993).
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Disteche C.M.;
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                                                                                                                                                                                                                                    SEQUENCE OF 41-102 AND 126-138.

MEDLINE=90239555; PubMed=2159184;

Ross T.S., Tait J.F., Majerus P.W.;

Ross T.S., Tait J.F., Majerus P.W.;

"Identity of inositol 1,2-cyclic phosphate 2-phosphohydrolase
lipocortin III.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Chromosomal localization of the human annexin III
                                                                                                                        Tait J.F., Sakata M., McMullen B.A., Miao C.H., Funakoshi
Hendrickson L.E., Fujikawa K.;
                                                                                                                                                               SEQUENCE OF 41-79; 85-88; 104-119; 126-150 AND MEDLINE=89118212; PubMed=2975506;
                                                                                                                                                                                                                     Science 248:605-607(1990)
                                                                                              "Placental anticoagulant proteins: characterization four members of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10:441-448(1991).
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Primates;
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Catarrhini; Hominidae
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                                                                                                                   comparative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anticoagulant
ol 1,2-cyclic
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CONFLICT
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REPEAT
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ProDom; PD000143; Annexin
SMART; SM00335; ANX; 4.
                                                                                                                                                                                                                                                                                                      SWISS-2DPAGE; P12429; HUMAN.
Aarhus/Ghent-2DPAGE; 5205; IEF
PMMA-2DPAGE; P12429; -.
                                                                                                                                                                                                                                                                                                                                                                     EMBL; M20560; AAA59496.1; -.
EMBL; M63310; AAA52284.1; -.
EMBL; L20591; AAA16713.1; -.
EMBL; BC000871; AAH00871.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cargill M.,
Shaw N., Lar
                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                      Annexin;
                                                                                                                                                                                                                                                         Pfam; PF00191; annexin;
                                                                                                                                                                                                                                                                                              Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                       InterPro; IPR001464; Annexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cargill M., Altshuler D., Ireland J., Sklar P., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., N Friedland L., Rolfe A., Warrington J., Lipshutz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The high-resolution crystal structure of human annexin III shows subtle differences with annexin V."; Biochemistry 35:1740-1744(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lander E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Friedland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS ASN-19; ASN-219; LEU-251 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99318093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization of single-nucleotide polymorphisms in coding regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lander E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human genes.";
t. Genet. 22:231-238(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     calcium and phospholipid.
SIMILARITY: Belongs to the annexin family.
SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Inhibitor of phospholipase A2, also possesses anti-
coagulant properties. Also cleaves the cyclic bond of inssitol
1,2-cyclic phosphate to form inositol 1-phosphate.
                                                                                                                                                                                                                                                                                                                                       1AXN; 08-MAR-96.
1AII; 12-MAR-97.
                                                                                                                                                                                                                                                                                   106490;
                                                                                                                                                                                                                                                                                                                                                               A47658; LUHU3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBs outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genet.
                                                                                                                                                                                                                                                                                        HGNC:541; ANXA3.
                                                                                                                                                                                            Lipase
                                                                                                                                                                                                     Calcium,
                                                                                                                                                                                                               PS00223; ANNEXIN; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lane
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Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra
L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
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183
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                                                                                                                                                                                         /phospholipid-binding;
inhibitor; 3D-structur
                                                                                                                                                                                                                                    Annexin; 4.
146
294
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17
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159
                                                                                                                                                                                        3D-structure;
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                                                    F -> S (in
/FTId=VAR_
                                                                          I -> N (in dbSNP:5948)
/FTId=VAR_013915.
P -> L (in dbSNP:5949)
/FTId=VAR_013916.
                                                                                                          /FTId=VAR_013914.
I -> N (in dbSNP:5948).
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                                                                                                                                 -> N (in dbSNP:5951)
                       dbSNt
.AR 013917.
G (IN REF.
R (IN PT
                                                                (in dbSNP:5941).
                                                                                                                                                                                                  Repeat;
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                              REF. 6).
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                                                                                                                                                                                       Polymorphism
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Nemesh J., Ziaugra
z R., Daley G.Q.,
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Ziaugra L.,
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Best Local
                                                                                     15-JUL-1999 (Rel. 38, C
15-JUL-1999 (Rel. 38, L
10-CCT-2003 (Rel. 42, L
Annexin A3 (Annexin III
protein III) (PAP-III)
                                                                                                                                               LT 24
MOUSE
MEDLINE=98172733; PubMed=9511742;
Fernandez M.P., Copeland N.G., Gilbert
Morgan R.O.;
                       SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                       Mus musculus
                                                                                                                      035639;
15-JUL-1999
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                                              NCBI_TaxID=10090;
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                                                                                                                                                                                                                                            RWGTDEDKFTEILCLRSFPQLKLTFDEYRNISQKDIVDSIKGELSGHFEDLLLAIVNCVR
                                                                                                                                                                                                                                                            KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                                                                                                                                                                                                                                                                           SQAYYTVYKKSLGDDISSETSGDFRKALLTLADGRRDESLKVDEHLAKQDAQILYKAGEN
                                                                                                                                                                                                                                                                                            KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL
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                                                                                                                                                                                                                                                                                                                                                            RGTVTDFFGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                                                                                                                                                                                                            KDDLKGDLSGHFEHLMVALVTPPAVFDAKQLKKSMKGAGTNEDALIEILTTRTSRQMKDI
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                                                                        (Mouse).
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                                                      Chordata;
Rodentia;
                                                                                            8, Last sequence update)
2, Last annotation update)
111) (Lipocortin III) (Placental
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185
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136
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160
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                                                                                                                       Created)
                                                                                       (35-alpha
                                                                                                                                                                               323
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                                                     Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                      Score 811;
Pred. No. 9
                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                      calcimedin)
                                                                                                                                      323
     D.J.,
                                                                                                                                                                                                                                                                                                                                                                                     9.7e-46;
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                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
     Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                            Length 323;
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                                                     Euteleostomi; 
Murinae; Mus
                                                                                             anticoagulant
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RESULT 25
ANX3 ANX3
AC P1466
DT 01-AI
DT 10-OA
DT 10-OA
DT 10-OA
DT Annes
DE Annes
DE Prott
GN ANXA
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Best Local S
Matches 157
P14669;
01-APR-1990 (Rel. 14, Createu,
01-APR-1990 (Rel. 14, Last sequence update,
10-OCT-2003 (Rel. 42, Last annotation update)
Annexin A3 (Annexin III) (Lipocortin III) (Placental
protein III) (PAP-III) (35-alpha calcimedin).
ANXA3 OR ANX3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (some send an email to license@isb-sib.ch).
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Gene 207:43-51(1998).
-i- FUNCTION: Inhibitor of phospholipase A2, also possesses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00196; ANNEXIN. ProDom; PD000143; Annexin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
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                                                                                                                                                    ANX3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: A pair of annexin repeats may calcium and phospholipid.
SIMILARITY: Belongs to the annexin fan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 4 annexin repeats.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
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                                                                                                                                                                                                                                           GDYRTVLLKICGEDD
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323
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                                                                                                                                                         STANDARD;
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159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
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Pred. No. 1.
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homology with lipocortin I.";
J. Biol. Chem. 263:10799-10811(1988).
-!- FUNCTION: Inhibitor of phospholipase A2, also
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
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ProDom; PD000143; Annexin; 4.
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Pfam; PF00191; annexin; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Ev
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sky R.B., Tizard R., Mattaliano R.J., Burne C., Huan
r G.T., Browning J.L., Chow E.P., Burne C., Huan
r G.T., Wachter L., Hession C., Frey A.Z., Wallner
distinct calcium and phospholipid binding prote
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ANNEXIN 4.
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Sciurognathi; Muridae;
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Search completed: March 25, 2004, 08:05:21 Job time : 19 secs

us-09-787-923-2.rsp

Page 22

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

March 25, 2004, 08:01:25; Search time 20 Seconds (without alignments) 1539.064 Million cell updates/sec

Perfect score: 1 MAQVLRGTVTDFPGFDERAD.....KGDTSGDYKKALLLLCGEDD 320 US-09-787-923-2 1600

Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100:

summaries

Database : : PIR_78:* pir2:*
pir3:*
pir4:* pir1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length		BB	ID	Description
1	1600	100.0	320	Н	AQHUP	۷ ۲
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7	931	58.2	318	H	LUPG4	annexin IV - Pig
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22	708.5	44.3	339	۲	TOHO36	11 - 5
23	706	44.1	512	N	S70644	annexin VII - ALLI
24	706	44.1	676	N	S41022	LICAL
25	704.5	44.0	339	_	LUBO36	; <u>-</u>
26	703.5	44.0	339	N	S33700	1 1
27	701.5	43.8	339	Н	LUMS 3 6	11
28	692.5	43.3	341	N	S55277	: :
29	688.5	43.0	340	1	JQ1298	annexin ii type 2

myosin heavy GP80 precurso lipid-binding

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annexin - pepp annexin-like p hypothetical p annexin p35 -annexin homolo

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annexin P33 probable annes

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annexin II - (
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endonexin - bo

annexin - upla

probable anne fiber annexin

ALIGNMENTS

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A; Reference number: A92696;
                                                                                                              A;Molecule type: protein
A;Residues: 86-131,'W',260-272,274-297,300-315,'X',317-320 <SCH>
R;Ahn, N.G.; Teller, D.C.; Bienkowski, M.J.; McMullen, B.A.; Lipkin,
J. Biol. Chem. 263, 18657-18663, 1988
                                                                  A; Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase A-
                                                                                                                                                                                                                                                                        A; Accession: A28038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: S01016; MUID:88271329; PMID:2455636
A;Accession: S01016
A;MOID:88271329; PMID:2455636
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A;Residues: 1-320 <FU
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R;Maurer-Pogy, I.; Reutelingsperger, C.P.M.; Pieters, J.; Bodo, G.; Stratowa, C.; Hauptr
Edit J. Bjochem. 174, 585-592, 1988
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R;Grundmann, U.; Abel, K.U.; Bohn, H.; Loebermann, H.; Lottspeich, F.; Kuepper, H
Proc. Natl. Acad. Sci. U.S.A. 85, 3708-3712, 1988
A;Title: Characterization of CDNA encoding human placental anticoagulant protein
A;Reference number: A30206; MUID:88234495; PMID:2967495
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A; Residues: l-320 <MAU>
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A; Title: Cloning and expression of cDNA for human endonexin
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                                                                                                                                                                                                                                                                                                                                                             "Molecule type: mRNA
"Residues: 1-320 <IWA-
"Residues: 1-320 <IWA-
"Ross-references: GB:D00172; NID:g219480; PIDN:BAA00122.1; PID:g219481
"Note: part of this sequence was confirmed by protein sequencing
"Note: part of this sequence was confirmed by protein sequencing
"Schlaepfer, D.D.; Mehlman, T.; Burgess, W.H.; Haigler, H.T.
roc. Natl. Acad. Sci. U.S.A. 84, 6078-6082, 1987
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                                                                                                                                                                                                                                                                                                  Reference number: A28038; MUID:87317598; PMID:2957692
                                                                                                                                                                                                                                                                                                                            Title: Structural and functional characterization of endonexin II, a calcium-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Title: Structure and expression of cDNA for an inhibitor of blocd coagulation isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Title: Primary structure of human placental anticoagulant protein. Reference number: A29417; MUID:88163463; PMID:2964863
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. Biol. Chem. 263, 8037-8043, 1988
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;Title: Five distinct calcium and phospholipid binding proteins share homology with li
;Reference number: A92659; MUID:88273202; PMID:2968983
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;Residues: 1-320 <GRU>
;Cross-references: GB:M19384; NID:g189614; PIDN:AAB59545.1; PID:g189615
;Cross-references: GB:M19384; NID:g189614; PIDN:AAB59545.1; PID:g189615
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Accession: D39250; A30206; A28076; S01016; A29417; A41514; A28038; C31953; S06646; A29;
Pepinsky, R.B.; Tizard, R.; Mattaliano, R.J.; Sinclair, L.K.; Miller, G.T.; Browning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: A29417
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       MUID:89066652; PMID:2974032
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F;249-320/Domain: annexin repeat homology <AX4>
F;249-320/Domain: annexin repeat homology <AX4>
F;260-276/Region: endonexin fold #status predicted
F;260-276/Region: endonexin fold #status predicted
F;27/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F;23/Binding site: phosphate (Thr) (covalent) #status predicted
F;28,30,32,72/Binding site: calcium, high affinity (Thr, Glu, Glu) #status experimental
F;33,35,36/Binding site: calcium, low affinity (Leu, Glu) #status experimental
F;73,78/Binding site: calcium, low affinity (Leu, Glu) #status experimental
F;100,102,104,144/Binding site: calcium, high affinity (Met, Gly, Asp) #status experimental
F;100,102,104,144/Binding site: calcium, high affinity (Met, Gly, Asp) #status experimental
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A;Introns: 3/3; 32/1; 63/3; 101/3; 132/1; 158/3; 177/3; 209/1; 241/1; 260/3; 301/3
C;Kuperfamily: annexin I; annexin repeat homology
C;Keywords: acetylated amino end; anticoagulant; calcium binding; duplication; endonexin F;2-320/Product: annexin V #status experimental <MAT>
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F;185-201/Region: endonexin fold #status predicted
F;249-320/Domain: annexin repeat homology <AX4>
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A;Title: The gene encoding human annexin V has a TATA-less promoter with a high G+C cont A;Reference number: 137172; MUID:95047484; PMID:7958998
A;Accession: 137172
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A;Residues: 29-73;274-297;300-320 <FU2>
R;Fernandez, M.P.; Morgan, R.O.; Fernandez, M.R.; Carcedo,
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A;Contents: annotation; X-ray crystallography, 2.0 angstroms
A;Note: three calcium ions are strongly bound at sites in the first, second,
R;Funakoshi, T.; Heimark, R.L.; Hendrickson, L.E.; McMullen, B.A.; Fujikawa,
Biochemistry 26, 5572-5578, 1987
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C;Comment: Annexins undergo reversible, calcium-dependent binding to membr
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A; Residues: 1-320 < R
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A;Residues: 7-25;27-42;51-74,'X',76-151;181-198;202-207;209-226;228-238;246-271;277-282,
R·H·her. R.: Schneider, M.; Mayr, I.; Roemisch, J.; Paques, E.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GDB:120555; OMIM:131230
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R;Rothhut, B.; com
J. 263, S
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BS Lett. 275, 15-21, 1990
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                                                                                                                                                                     MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
                                          FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
                                                                                                                              MAQVLRGTVTDFFGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
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Pred. No. 3.7e-96;
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ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF 180

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A; Alternate names: CaBP33; CaBP37

N; Alternate names: CaBP33; CaBP37

C; Species: Bos primigenius taurus (cattle)

C; Species: Bos primigenius taurus (cattle)

C; Accession: S27214; S27215

C; Accession: S27214; S27215

Biochim. Biophys. Acta 1160, 76-83, 1932

A; Title: Novel isoforms of CaBP 33/37 (Annexin V) from mammalian brain: structural and p A; Reference number: S27214; MUID:93041974; PMID:1420335

A; Recession: S27214

A; Molecule type: protein
A; Accession: S27215

A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-320 < LEA>
A; Molecule type: protein
A; Residues: 1-35, 'T', 37-124, 'E', 126-320 < LE2>
A; Note: It is uncertain whether the sequence differences are due to allelic variation or A; Note: It is uncertain whether the sequence differences are due to allelic variation or A; Note: It is uncertain whether the sequence differences are due to allelic variation or A; Note: It is uncertain whether the sequence differences are due to allelic variation or A; Note: It is uncertain whether the sequence differences are due to allelic variation or A; Note: It is uncertain whether the sequence differences are due to allelic variation or A; Note: It is uncertain whether the sequence differences are due to allelic variation or A; Note: It is uncertain whether the sequence differences are due to allelic variation or A; Note: It is uncertain whether the sequence differences are due to allelic variation or A; Note: It is uncertain whether the sequence differences are due to allelic variation or A; Note: It is uncertain whether the sequence differences are due to allelic variation or A; Note: It is uncertain whether the sequence differences are due to allelic variation or A; Note: It is uncertain whether the sequence differences are due to allelic variation or A; Note: It is uncertain whether the sequence differences are due to allelic variation or A; Note: It is uncertain whether It is uncertain whether It is uncertain whether It is uncertain whether It is uncertain whether It is uncertain whe
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F;28.44/Region: endomexin fold #status predicted
F;89-160/Domain: annexin repeat homology cAX2>
F;100-116/Region: endomexin fold #status predicted
F;100-116/Region: endomexin fold #status predicted
F;102-244/Domain: annexin repeat homology cAX3>
F;184-200/Region: endomexin fold #status predicted
F;248-319/Domain: annexin repeat homology cAX4+
F;258-275/Region: endomexin fold #status predicted
F;27/Region: endomexin fold #status predicted
F;22/Binding site: acetylated amino end (Ala) #status experimental
F;27/Binding site: calcium, low affinity (Met, Gly, Gly, Glu) #status predicted
F;27,79,31,71/Binding site: calcium, low affinity (Thr, Glu, Glu) #status predicted
F;23,34,35/Binding site: calcium, low affinity (Leu, Glu, Gly, Asp) #status predicted
F;29,101,103,143/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status predicted
F;258,260,262,302/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status predicted
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                                                                                                          LRAIKQVYEEBYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQ 181
                                                                                                                                                                                                       AGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVV 241
                                                                    <u>LRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDARIDEAQVEQDAQALFQ</u>
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96.9%; Pred. No: 1.2e-92;
tive 5; Mismatches 4
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g Qy	Query Best Match	# 1 2 6 8 7 1 2 6 8 7 1 2 6 8 7 1 2 8	C; Keywo C; Keywo C; Keywo C; Keywo F; 2-31 F; 27.4 F; 28.1 F; 188.1 F; 183.1 F; 183.1 F; 183.1 F; 183.1	C;Comment: Olipid-bin C;Genetics	A; Accession A; Status: p A; Molecule A; Residues: A; Cross-ref C; Comment:	A; Cross R; Imai Eur. J A; Titl A; Refe	LURT5 Annexin V - N;Alternate C;Species: 1 C;Date: 30-: C;Accession R;Pepinsky, J, Biol. Ch A;Title: Fi A;Reference A;Accession A;Molecule A;Residues: A;Cross-ref	QY Db RESULT	
5 LRGTV 3 LRGTV	Match Local S es 292	28-2/4/kegion: endougate calcium, 126,28,30,70/Binding site: calcium, 10w 31,33,34/Binding site: calcium, low 71,76/Binding site: calcium, low aff;98,100,102,142/Binding site: calcium;98,267,259,261,301/Binding site: calcium;257,259,261,301/Binding site: calcium;257,259,261	A;Introns: 1/3; 30/1; 6 C;Superfamily: annexin C;Keywords: calcium bin F;2-319/Product: annexin F;2-319/Product: annexin F;27-43/Region: endonex F;88-159/Domain: annexi F;99-115/Region: endone F;171-243/Domain: annexi F;183-199/Region: endor F;183-199/Region: endor	ent: Annexin V -binding rathe tics:	A; Accession: wholey A; Status: preliminary; A; Molecule type: DNA A; Residues: 1-319 < IMA A; Cross references: EM C; Comment: Annexins un	R;Imai, Y; Kohsaka, S. R;Imai, Y; Kohsaka, S. Eur. J. Biochem. 232, 327-334, 1995 A;Title: Structure of rat annexin V gene and molecular of the structure of	IURT5 annexin V - rat annexin V - rat c;Species: Rattus norvegicus (Norway rat) c;Species: Rattus norvegicus (Norway rat) c;Accession: C29250; S66680 c;Accession: C29250; S66680 g;Repinsky, R.B.; Tizard, R.; Mattaliano, R.J.; J. Biol. Chem. 263, 10799-10811, 1988 J. Biol. Chem. 263, 10799-10811, 1988 A;Title: Five distinct calcium and phospholipid A;Reference number: A92659; MUID:88273202; PMID: A;Accession: C29250 A;Accession: C29250 A;Accession: C29250 A;Accession: C39269: mRNA A;Residues: 1-319 <pep> A;Cross-references: GB:M21730; NID:g205138; PIDN A;Cross-references: GB:M21730; NID:g205138; PIDN A;Cross-references: GB:M21730; NID:g205138; PIDN</pep>	302 GDTSGD 301 GDTSGD	
LRGTVTDFEGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQE SAAFKILFG	91.5%; larity 92.1%; Conservative	, region: endough. The color works, region; (A), region; (A), region; (A), roll affinity (Met, Gly, Gly, 0,70/Binding site: calcium, low affinity (Thr, Glu, Asp) #8 sinding site: calcium, low affinity (Leu, Glu, #status pr 102,142/Binding site: calcium, high affinity (Leu, Gly, 261,301/Binding site: calcium, high affinity (Met, Gly, 261,301/Binding site: calcium, high affinity (Met, Gly, 1,261,301/Binding site: calcium	/3; 30/1; 61/3; 99/3; 130/1; 150/3; 150/3; y: annexin I annexin repeat homology calcium binding; duplication; endonexin htt: annexin V #status predicted «MAT» hin: annexin repeat homology «AXI» in: annexin fold #status predicted nain: annexin repeat homology «AX2» jion: endonexin fold #status predicted sgion: endonexin fold #status predicted sgion: endonexin fold #status predicted sgion: annexin repeat homology «AX3»	V has been proposed her than proteolytic	nary; translation DNA <ima> s: EMBL:D42136</ima>	2, 327-334, 1 of rat annexi s66680; MUID	endonexin II; norvegicus (No) 2 #sequence_rev 0; \$56680 Tizard, R.; Mat Tizard, R.; Mat Tizard, R.; Mull 1: A92659; MUID 10 10 10 10 10 10 10 10 10 10 10 10 10	GDTSGDYKKALLLLCGGEDD	
ETLRKAMKGLGTI EVLRKAMKGLGTI	; Score 1464.5; ; Pred. No. 2e-8 12; Mismatches	rium, high affinin, low affinity low affinity calcium, high calcium, high	mnexin repeat homology; iii) duplication; endonexi; iii) duplication; endonexi; iiii) endonexi iiii) endonexi iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii		lation not shown 136 reversible, calc	995 n V gene and :96035863; PN	; lipocortin vorway rat) evision 30-Sep attaliano, R.J attaliano, R.J and phospholip b:88273202; Pv D:88273203; Pv		
DEESILTLLTSR	1.5; DB 1; 2e-87; thes 12;	finity (Met, ty (Thr, Glu) f (Leu, Glu) f n affinity (I h affinity	homology ; endonexin fold cted (MAT) <ax1) redicted redicted predicted predicted predicted y <ax3) predicted s predicted</ax3) </ax1) 	a role ir tion. It	hown 	molecular d MID:7556178	lacental 92 #text Sinclair binding 2968983		
SNAQRQEISAAL	Length 319; Indels 1;	Gly, Gly, Glu, Glu, Asp) #status #status predict Leu, Gly, Gly, (Met, Gly, Gly,	i i	the inhi does not	bin	diversity of	change 22-Jun L.K.; Miller proteins share		TDRETSGNLEQ
KTLFG	Gap	Gly, Glu) #status p predicted y, Gly, As ly, Gly, A	0	bition caffect t	3	its t	pulant pr ;2-Jun-19 ;iller, G ;share ho		LYSMIF

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F;2-321/Product: annexin v #status predicted
F;29-45/Region: endonexin fold #status predicted
F;99-45/Region: endonexin fold #status predicted
F;90-161/Domain: annexin repeat homology <AX2>
F;101-117/Region: endonexin fold #status predicted
F;103-245/Domain: annexin repeat homology <AX3>
F;105-201/Region: endonexin fold #status predicted
F;249-320/Domain: annexin repeat homology <AX4>
F;260-276/Region: endonexin fold #status predicted
F;28,30,32,72/Binding site: calcium, high affinity (Met, Glu, Glu) #status predicted
F;33,78/Binding site: calcium, low affinity (Thr, Glu, Glu) #status predicted
F;73,78/Binding site: calcium, low affinity (Leu, Glu) #status predicted
F;73,78/Binding site: calcium, low affinity (Leu, Glu) #status predicted
F;73,78/Binding site: calcium, low affinity (Leu, Glu) #status predicted
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Blochem. J. 291, 601-608, 1993
A;Title: Isolation, Characterization and localization of annexin V from chicken liver.
A;Reference number: S32523; MUID:93249384; PMID:8484740
A;Accession: S32523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 6-20;85,'X',87-88,'X',90-93,'X',95-96,'XX',99-100,'X',102-103,'XX',106-107;
C;Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 02-Jun-2000
C.Accession: A35381, A28623; B40404; S32523; S08771
C.Accession: A35381, A28623; B40404; S32523; S08771
R.Fernandez, M.P.; Selmin, O.; Martin, G.R.; Yamada, Y.; Pfaeffle, M.; Deutzmann, J. Biol. Chem. 265, 8344, 1990
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A;Reference number: A35381; MUID:90243721; PMID:2159478
A;Contents: erratum
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F;377-393/Region: endonexin rolu mouler cax6>
F;438-509/Domain: annexin repeat homology cax6>
r:449-465/Region: endonexin fold #status predicted
                                                                     F;527-598/Domain:
F;538-554/Region:
                                                                                                                                                                                             F;178-250/Domain: annexin repeat homology <AX3>
F;190-206/Region: endonexin fold #status predicted
F;254-325/Domain: annexin repeat homology <AX4>
F;265-281/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: annexin VI; annexin repeat homology C;Keywords: acetylated amino end; calcium binding; F;2-673/Product: annexin VI #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-673 <MOS>
A;Cross-references: EMBL:X13460; NID:g53580; PIDN:CAA31808.1; PID:g53581
A;Note: the authors translated the codon GCC for residue 329 as Gly
C;Comment: This abundant cytosolic protein binds to the inner surface of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N/Alternate names: calcium-binding protein p68; calelectrin; calphobindin II C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1989 #sequence_revision 26-May-1994 #text_change 22-Jun-1999 C;Accession: S01786 R;Moss, S.E.; Crompton, M.R.; Crumpton, M.J.
        F;613-629/Region: F;2/Modified site:
                                                                                                                                                 F;366-437/Domain: annexin repeat homology <AX5>
F;377-393/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                       F;95-166/Domain: annexin repeat homology <AX2>F;106-122/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                   F;23-94/Domain: annexin repeat homology <AX1>
F;34-50/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Molecular cloning of murine p68, a Ca-binding A;Reference number: S01786; MUID:89030687; PMID:2972541 A;Accession: S01786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eur.
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S01786
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annexin repeat homology <AX8>
endonexin fold #status predicted
acetylated amino end (Ala) (in
                                                                  annexin repeat homology <AX7>
endonexin fold #status predicted
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  (in mature form) #status
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Local

Similarity

59.4%;

Score 942; DB 1; Pred. No. 2.7e-53

DB 1;

Length 673;

Indels

0,

Gaps

0,

Conservative

49;

Mismatches

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C;Species: Homo sapiens (man)
C;Date: 30-Jan-1993 #sequence revision 26-May-1994 #text_change 22-Jun-1999
C;Accession: A42077; B42077; S07434; A31953; A31046
R;Tait, J.F.; Smith, C.; Frankenberry, D.A.; Miao, C.H.; Adler, D.A.; Disteche, Genomics 12, 313-318, 1992
A;Title: Chromosomal mapping of the human annexin IV (ANX4) gene.
A;Beference number: A42077; MUID:92155721; PMID:1346776
A;Accession: A42077.
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A;Molecule type: mRNA
A;Residues: 1-97,'0','99-321 <GRU>
A;Residues: 1-97,'0','99-321 <GRU>
A;Cross-references: EMBL:M19383; NID:g189616; PIDN:AAC41689.1; PID:g189617
A;Choss-references: EMBL:M19383; NID:g189616; PIDN:AAC41689.1; PID:g189617
A;Choss-references: EMBL:M19383; NID:g189616; PIDN:AAC41689.1; PID:g189617
A;Choss-references: EMBL:M19383; NID:g189616; PIDN:AAC41689.1; PID:g189617
A;China (Company)
A;Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase
A;Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Grundmann, U.; Amann, E.; Abel, K.J.; Kuepper, H.A. Behring Inst. Mitt. 82, 59-67, 1988
A;Title: Isolation and expression of cDNA coding for a new A;Reference number: S07434; MUID:88309022; PMID:2970257
A;Accession: S07434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: endonexin I; placental anticoagulant protein II; PP4-X
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A;Accession: B42077
                                                                                                                                                                                                                                     A;Residues: 29-58;101-126;282-310 <AHN>
R;Tait, J.F.; Sakata, M.; McMullen, B.A.; Miao, C.H.; Funakoshi, T.; Hendrickson, L.E.; Biochemistry 27, 6268-6276, 1988
A;Title: Placental anticoagulant proteins: isolation and comparative characterization o. A;Reference number: A90534; MUID:89118212; pMID:2975506
                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A92696; MUID:89066652; A;Accession: A31953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type:
                                                                                                                                                          A;Molecule type: protein
A;Residues: 4-17;30-74;102-146;283-321 <TA3
                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 29-58; 101-120
                                                       A; Map position: 2p13-2p13
                                                                                                         A; Gene: GDB: ANX 4
                                                                                                                                                                                                                  A; Accession: A31046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 1-321 <TAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: mRNA
                                                                             ;Cross-references:
:Superfamily: annexin I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGTYTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STPEYFAERLFKAMKGLGTRONTLIRIMVSRSELDMLDIREIFRTKYEKSLYSMIKNDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEYKKALLKLCGGDD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDYKKALLLLCGEDD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
                                                                             GDB:131395; OMIM:106491
           annexin
           repeat homology
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F;247-318/Domain: annexin repeat homology <AX4>
F;258-274/Region: endonexin fold #status predicted
F;17604ffied site: blocked amino end (Ala) (probably acetylated)
F;6/Binding site: phosphate (Thr) (covalent) (by protein kinase C
F;124,244/Binding site: carbohydrate (Asn) (covalent) #status pre

ر) #status ع C) #-

F;88-159/Domain: annexin repeat homology <AX2>
F;99-115/Region: endonexin fold #status predicted
F;171-243/Domain: annexin repeat homology <AX3>
F;183-199/Region: endonexin fold #status predicted

C;Superfamily: annexin 1; annexin repeat non-co; C;Keywords: blocked amino end; calcium binding; F;16-87/Domain: annexin repeat homology xAXI>

#status predicted

duplication;

endonexin

ç

men

Superfamily: annexin I; annexin repeat homology 16-87/Domain: annexin repeat homology <AX1> 27-43/Region: endonexin fold #status predic

derstood

A;Molecule type: protein A;Residues: 1-318 <WEB> A;Experimental source: intestinal epithelium C;Comment: Annexins undergo reversible, calcium-dependent binding

U.; Van, P.N.; Soling, H.D.; Ampe,

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F;247/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;247/Binding site: carbohydrate (Asn) (covalent) #status predicted
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G;Date: 30'-0; 22107
G;Accession: A27107
C;Accession: A27107
R;Weber, K.; Johnsson, N.; Plessmann, U.; Van, P.N.; Soling, H.U., ....r
R;Weber, K.; Johnsson, N.; Plessmann, U.; Van, P.N.; Soling, H.U., ....r
EMBO J. 6, 1599-1604, 1987
A;Title: The amino acid sequence of protein II and its phosphorylation
A;Title: The amino acid sequence of protein II and its phosphorylation
A;Title: The amino acid sequence of protein II and its phosphorylation
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                                                                                                                                                                                                                                                  N;Alternate names: 32K calelectrin; chromobindin IV; endonexin; lipocort C;Species: Sus scrofa domestica (domestic pig) (C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 24-Nov-1
                                                                                                                                                                                                                                                                                                                                                   annexin IV - pig
N;Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-90/Domain: annexin repeat homology <AX1>30-46/Region: endonexin fold #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Keywords: acetylated amino end; calcium binding; duplication; endonexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;247/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174-246/Domain: annexin repeat homology <AX3>
;186-202/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;102-118/Region: endonexin fold #status predicted
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Pred. No. 4.1e-53;
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A;Cross-references: EMBL:X86086; NID:g763180; PIDN:CAA60040.1; PID:g763181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Fan, H.; Josic, D.; Lim, Y.P.; Reutter, W.
Eur. J. Biochem. 230, 741-751, 1995
A;Title: CDNA cloning and tissue-specific regulation of expression of rat calcium-bindin A;Reference number: S65683; MUID:95331313; PMID:7607247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: calcium-binding protein 65/67 C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449-465/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :377-393/Region:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keywords: acetylated amino end; calcium binding;
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Best Local
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                                                                                                                                                   Local Similarity es 186; Conserv
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                  RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAF/KTLFGRDL 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDLKSELSGNFEQVILGMMTÞTVLÝÐVQELRRAMKGAGTDEGCLIEILASRÍÞEEIRRÍN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 126
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endonexin fold
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endonexin fold
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                                                                                                                                                                            59.0%;
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58.9%;
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                                                                                                                                    Score 931; DB 1; 1
Pred. No. 1.4e-52;
8; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                             homology <AX8>
                                                                                                                                                                                                                                                                                                                                                                                              #status predicted
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Pred. No. 5.4e-53;
51; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endonexin fold; membrane-associated
                                                                                                                                                                                                      Length 673;
                                                                                                                                        Indels
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                                                                                                          A;Title: Characterizations of two distinct Ca(2+)-dependent phospholipid-binding protein A;Reference number: A34459; MUID:90008880; PMID:2529258
                                                                                                                                                                         A;Molecule type: protein
A;Residues: 2-299;307-314;320-445;447-549;581-673
A;Residues: 2-299;307-314;320-445;447-549;581-673
A;Residues: 2-299;307-314;320-445;447-549;581-673
A;Residues: 2-299;307-314;320-445;447-549;581-673
A;Residues: 2-299;307-314;320-445;447-549;581-673
A;Residues: 2-299;307-314;320-445;447-549;581-673
A;Residues: 2-299;307-314;320-445;447-549;581-673
A;Residues: 2-299;307-314;320-445;447-549;581-673
A;Residues: 2-299;307-314;320-445;447-549;581-673
A;Residues: 2-299;307-314;320-445;447-549;581-673
A;Residues: 2-299;307-314;320-445;447-549;581-673
A;Residues: 2-299;307-314;320-445;447-549;581-673
A;Residues: 2-299;307-314;320-445;447-549;581-673
A;Residues: 2-299;307-314;320-445;447-549;581-673
A;Residues: 2-299;307-314;320-445;447-549;581-673
A;Residues: 2-299;307-314;320-445;447-549;581-673
A;Residues: 2-299;307-314;320-445;447-549;581-673
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A;Residues: 2-299;307-314;320-445;447-549;581-673
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A;Residues: 2-299;307-314;320-445;447-549;581-673
A;Residues: 2-299;307-445;447-549;581-673
A;Residues: 2-299;307-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;407-45;
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A;Molecule type: mRNA
A;Residues: 1-225; 'MK', 228-554,'T', 556-673 <SUE>
A;Cross-references: GB:J03578; NID:g179975; PIDN:AAA35656.1; PID:g17
A;Cross-references: GB:J03578; NID:g179975; PIDN:AAA35656.1; PID:g17
A;Cross-references: GB:J03578; NID:g179975; PIDN:AAA35656.1; PID:g17
A;Cross-references: GB:J03578; NID:g179975; PIDN:AAA35656.1; PID:g17
A;Cross-references: GB:J03578; NID:g179975; PIDN:AAA35656.1; PID:g17
A;Cross-references: GB:J03578; NID:g179975; PIDN:AAA35656.1; PID:g17
A;Cross-references: GB:J03578; NID:g179975; PIDN:AAA35656.1; PID:g17
A;Cross-references: GB:J03578; NID:g179975; PIDN:AAA35656.1; PID:g17
A;Cross-references: GB:J03578; NID:g179975; PIDN:AAA35656.1; PID:g17
A;Cross-references: GB:J03578; NID:g179975; PIDN:AAA35656.1; PID:g17
A;Cross-references: GB:J03578; NID:g179975; PIDN:AAA35656.1; PID:g17
A;Cross-references: GB:J03578; NID:g179975; PIDN:AAA35656.1; PID:g17
A;Cross-references: GB:J03578; NID:g179975; PIDN:AAA35656.1; PID:g17
A;Cross-references: GB:J03578; NID:g179975; PIDN:AAA35656.1; PID:g17
A;Molecule type: protein
A;Residues: 10-25;69-75;136-151;192-207;209-220;300-306 <HAY>
                                                                                        A;Accession: B34459
                                                                                                                                                                                                                                                                                                                                                                    A;Title: Structure and properties of calphobindin II, an anticoagulant protein from A;Reference number: JX0091; MUID:90236978; PMID:2139657
                                                                                                                                                                                                                                                                                                                                              A; Accession: JX0091
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PID:g179976

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A;Residues: 103-113;167-172,'X',174-177;232-235,'F',237-240;251-258;277-281;359-362,'G', A;Note: the sequence from Fig. 6 is inconsistent with that from Fig. 4 in having 619-Glu A;Note: eight calcium ions are bound in the presence of phospholipid R;Suedhof, T.C.; Slaughter, C.A.; Leznicki, I.; Barjon, P.; Reynolds, G.A. Proc. Natl. Acad. Sci. U.S.A. 85, 664-668, 1988
A;Title: Human 67-kDa calelectrin contains a duplication of four repeats found in 35-kDa A;Reference number: A31079; MUID:88124902; PMID:2963335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: calcium-binding protein, 68K; calelectrin; calphobindin 1 C;Species: Homo sapiens (man) C;Date: 31-Mar-1992 #sequence revision 30-Sep-1992 #text_change 08-Dec-2000 C;Date: 31-Mar-1992 #sequence revision 30-Sep-1992 #text_change 08-Dec-2000 C;Accession: JU0032; S00263; S18519; A31079; JX0091; B34459; B31953; A53507 R;Twasaki, A.; Suda, M.; Watanabe, M.; Nakao, H.; Hattori, Y.; Nagoya, T.; %
                                                                                                                                                                                                                                                 A; Molecule type: protein
                                                                                                                                                                                                                                                                                         A; Accession: S18519
                                                                                                                                                                                                                                                                                                   A;Residues: 1-618,'D',620-673 <CR1>
A;Cross-references: EMBL:Y00097; NID:G35217; PIDN:CAA68286.1; PID:G35218
                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-618, 'D', 620-673
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Primary structure of the human, membrane-associated Ca(2+)-binding protein A;Reference number: S00263; MUID:88196081; PMID:3258820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Crompton, M.R.; Owens, R.J.;
EMBO J. 7, 21-27, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:D00510; NID:g219550; PIDN:BAA00400.1; PID:g219551
R;Crompton, M.R.; Owens, R.J.; Totty, N.F.; Moss, S.E.; Waterfield, M.D.; Crumpton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biochem. 106, 43-49, 1989
A;Title: Structure and expression of cDNA for calphobindin II, a human placental coagula
A;Reference number: JU0032; MUID:89380132; PMID:2528541
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S00263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KWGTDEAQFÍYÍLGNRSKQHLRLVFDEYLKTTGKPÍEASÍRGELSGDFEKLMLAVVKCÍR
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A;Experimental source: placenta
R;Ahn, N.G.; Teller, D.C.; Bienkowski, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, (
J. Biol. Chem. 263, 18657-18663, 1988
A;Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase
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A;Accession: B31953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Molecule type: protein
;Residues: 'X',473-480,'DY' <HYA>
;Comment: This abundant cytosolic
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                                                                                                                                KWGTDEAQFIYILGNRSKQHLRLVFDEYLKTTGKPIEASIRGELSGDFEKLMLAVVKCIR
                                                                                                 SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
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 GEYKKTLLKLSGGDD
                                  GDYKKALLLLCGEDD 320
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Pred. No. 2.5e-52;
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IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGD

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DYKKALLLLCGEDD 320

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N,Alternate names: 32K calelectrin; chromobindin IV; endonexin; lipocorti C;Species: Bos primigenius taurus (cattle) C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text change 22-Jun-19 C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text change 22-Jun-19 C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text change 22-Jun-19 C;Accession: A31578; D45066; B45066; C45066; F45066; G450 R;Hamman, H.C.; Gaffey, L.C.; Lynch, K.R.; Creutz, C.E. Biochem. Biophys. Res. Commun. 156, 660-667, 1988 A;Title: Cloning and characterization of a cDNA encoding bovine endonexin A;Reference number: A31578; MUID:89050088; PMID:2847715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. J. 312, 175-181, 1995
A, Title: Ca(2+)-dependent binding of annexin IV to surfactant protein A A; Reference number: S59624; MUID:96077142; PMID:7492310 | A, Accession: S59624
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A;Title: Carbohydrate-binding proteins in bovine kidney
A;Reference number: A45066; MUID:93015942; PMID:1400371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:X13627; NID:g215; PIDN:CAA31954.1; PID:g216; GB:M2
R;Kojima, K.; Ogawa, H.K.; Seno, N.; Yamamoto, K.; Irimura, T.; Osawa, T
J. Biol. Chem. 267, 20536-20539, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-319 < HAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   annexin IV -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 29-44;72-77;112-119;163-180;181-190;226-235 < SOH>
C;Comment: Annexins undergo reversible, calcium-dependent binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 10-18,'X',20-22,'X',24-25;29-48;101-107,'X',109-118;'X',194-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;28-44/Region: endonexin fold #status predicted F;89-160/Domain: annexin repeat homology <AX2> F;100-116/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Keywords: calcium binding; duplication; endonexin F_12-319/Product: annexin IV #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                              ;248-319/Domain: annexin repeat homology <AX4>;259-275/Region: endonexin fold #status predicted;7/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #stat;7/Binding site: carbohydrate (Asn) (covalent) #status predicted;125,245/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;172-244/Domain: annexin repeat ;184-200/Region: endonexin fold
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                       183;
  66 DDLKSELSGNFEQVILGMMTPTVLYDVQELRKAMKGAGTDE
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                                                                                                                  GTVKAASGFNAAEDAQTLRKAMKGLGTDEDAIINVLAYRSTAQRQEIRTAYKTTIGRI
                                                       DDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                  57.8%;
58.3%;
                                                                                                                                                                                                                                       51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homology <AX3>
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Pred. No. 1.5e-52;
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N;Alternate names: calcyclin-associated protein peptide, CAP-50 (;Species: Bos primigenius taurus (cattle) (;Cpecies: Bos primigenius taurus (cattle) (;Cpecies: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 22-Jun-1999 C;Accession: A42113; A42909; B42909; C42909; D42909 R;Towle, C.A.; Treadwell, B.V.
J. Biol. Chem. 267, 5416-5423, 1992
A;Title: Identification of a novel mammalian annexin. cDNA cloning, sequence A;Reference number: A42113; MUID:92184796; PMID:1372001
A;Cross-references: GB:M82802; NID:g162673; PIDN:AAA30379.1;
                                                                                                                                                                                                                                                                               annexin XI form A - bovine
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C;Superfamily: annexin VI; annexin repeat homology
C;Keywords: calcium binding; phospholipid binding
F;21-92/Domain: annexin repeat homology <AXI>
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F;252-323/Domain: annexin repeat homology <AX4>
F;364-435/Domain: annexin repeat homology <AX5>
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B;Title: Characterization, cloning and expression of the 67-kDa annexin from chicken A;Reference number: JC2029; MUID:94092130; PMID:8267590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: 67K lipid-dependent Ca2+-binding protein C;Species: Gallus gallus (chicken)
C;Date: 30-Sep_1993 #sequence_revision 20-Aug-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;93-164/Domain: annexin repeat homology <AX2>
                             ;Molecule type: mRNA;Residues: 1-503 <TOW>
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                                                                           ACCESSION: A42113
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Best Local S
Matches 185
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58.0%;
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                                                                                                         cDNA cloning, sequence analysis,
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PID:g162674
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A;Residues: 1-505 <TOW>
A;Residues: 1-505 <TOW>
A;Cross references: EMBL:Z11742; NID:g77; PIDN:CAA77801.1; PID:g78
R;Towle, C.A.; Weissbach, L.; Treadwell, B. Biochim. Biophys. Acta 1131, 223-226, 1992 A;Title: Alternatively spliced annexin XI t A;Reference number: S36136; MUID:92305067;
                                                                                                                                            A;Reference number: A;Accession: S23447
                                                                                                                                                                                                                                 annexin XI form B - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 22-Nov-1993 #sequence_revision 10-Feb-1995
                                                                                                                                                                                                                                                                                                            RESULT 13
S23447
                                                                                                                                                            submitted to the EMBL Data A; Reference number: S23447
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R;Towle, C.
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F;443-459/Region: endonexin fold #status predicted
F;59,111/Binding site: carbohydrate (Asn) (covalen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 19/1; 56/2
A;Note: the list of introns is incomplete
C;Superfamily: annexin VII; annexin repeat homology
C;Keywords: calcium binding; duplication; endonexin
F;201-272/Domain: annexin repeat homology <AXI
F;212-228/Kegion: endonexin fold #status predicted
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A;Experimental source: lung
A;Note: sequence modified after extraction from NCBI backbone
A;Note: sequence modified after extraction from NCBI backbone
Calcium-dependent binding to membrane
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A;Title: CAP-50, a newly identified annexin, localizes A;Reference number: A42909; MUID:92317074; PMID:1618851
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Best Local
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Pred. No. 3.9e-49;
                                                                                                                                                                                February 1992
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transcripts e; PMID:1535225
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A;Note: the list of introns is incomplete (Superfamily: annexin VII; annexin repeat homology C;Superfamily: annexin VII; annexin repeat binding; R;203-274/Domain: annexin repeat homology <AXI> F;203-274/Domain: endonexin fold #status predicted R;214-230/Region: endonexin repeat homology <AXI> F;286-302/Region: endonexin fold #status predicted R;286-302/Region: endonexin fold #status R;286-302/Region: endonexin fold #status R;286-302/Region: endonexin fold #status R;286-302/Region: endonexin fold #status R;286-302/Region: endonexin fold #status R;286-302/Region: endonexin fold #status R;286-302/Region: endonexin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: calcyclin-associated annexin protein CAP-50
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 16-Jun-2000
C;Accession: JH0694; PH0950; A38250; PS0263
R;Tokumitsu, H.; Mizutani, A.; Muramatsu, M.; Yokota, T.; Arai, K.; Hidaka, H.
Biochem. Biophys. Res. Commun. 186, 1227-1235, 1992
A;Title: Molecular cloning of rabbit CAP-50, a calcyclin-associated annexin protein.
A;Reference number: JH0694; MUID:92378579; PMID:1380798
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                                                                                   A;Molecule type: protein
A;Molecule type: protein
A;Residues: 104-141;213-231;254-262;270-280;285-309;319-337;429-448;478-492 <TK2>
R;Tokumitsu, H.; Mizutani, A.; Minami, H.; Kobayashi, R.; Hidaka, H.
R;Tokumitsu, H.; Mizutani, A.; Minami, H.; Kobayashi, R.; Hidaka, H.
J. Biol. Chem. 267, 8919-8924, 1992
                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-503 < TOK>
                                                                                                                                                                                                                                                                                                                          A;Cross-references: DDBJ:D10883; NID:g471147; PIDN:BAA01705.1; PID:g471148
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: JH0694
J. Biol. Chem. 267, 8919-8924, 1992
A;Title: A calcyclin-associated protein is a newly identified
A;Reference number: A38250; MUID:92250478; PMID:1533622
                                                                                                                                                                                                                                                   A; Accession: PH0950
                                                                                                                                                                                                                                                                                         A; Experimental source: lung
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Residues: 1-77 <TO2>
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A;Molecule type: protein
A;Residues: 104-141;213-223,'X',225-231;254-263;271-280;285-291,'X',293-3
C;Comment: This protein binds specifically to calcyclin in a Ca2+ depende
C;Comment: This protein binds specifically to calcyclin in a Ca2+ depende
C;Superfamily: annexin VII; annexin repeat homology
C;Keywords: calcium binding; duplication; endonexin fold; glycoprotein; p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A38250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;201-272/Domain: annexin repeat homology <AX1>
F;212-228/Region: endomexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;443-459/Region: annexin repeat homology <AX4>F;443-459/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;368-384/Region: endonexin fold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;356-428/Domain: annexin repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;284-300/Region: endonexin fold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;273-344/Domain: annexin repeat
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                                                                                                                                                                                                                                                                                                                R;Misaki, Y.; Pruijn, G.J.M.; van der Kemp, A.W.C.M.; van Venrooij, J. Biol. Chem. 269, 4240-4246, 1994
A;Title: The 56K autoantigen is identical to human annexin XI.
A;Reference number: A53152; MUID:94140847; PMID:7508441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 13-Aug-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Homo sapiens (man)
                                                                                                                           A;Gene: GDB:ANX11
A;Cross-references: GDB:313076
A;Map position: 9q11-9q22
                                                                                                                                                                                                           A;Cross-references: GB:L19605; NID:g457128; PIDN:AAA19734.1; PID:g457128
                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-505 < MIS>
                                                                                                                                                                                                                                                                                                 A; Accession: A53152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annexin XI -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
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                                     203-274/Domain: annexin repeat;275-346/Domain: annexin repeat
                                                                             Superfamily: annexin VII; annexin repeat homology; Reywords: calcium binding; duplication; endonexin
                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                        Status: preliminary
358-430/Domain:
434-505/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 RGTITDASGFDPLRDAEVLRKAMKGFGTDEQAIIDCLGSRSNKQRQQILLSFKTAYGKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 NKAYKTEFKKTLEEAIRSDTSGHFQRLLISLSQGNRDESTNVDMSLVQRDVQELYAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 RIGTDESKFNAVLCSRSRAHLVAVFNEYORWTGRDIEKSICREMSGDLEOGMLAVVKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDEDAGIDEAQYEQDAQALFQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66. LDDLKSELTGKPEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTPAFFAERLNRAMRGAGTKDRTLIRIMVSRSEIDLLDIRAEYKRMYGKSLYHDISGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKÉFRKNFATSLYSMIKGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDYKKALLLCGEDD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDYRKILLKICGGND
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  annexin
                        annexin
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54.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homology <AX2>
#status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 873; DB 1;
Pred. No. 5.2e-49;
                   homology <AX2>
homology <AX3>
    homology
                                                                  homology <AX1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
        <AX4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 503;
                                                                                          fold; glycoprotein;
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Query Match Best Local Similarity

> Score 865; DB 2; Pred. No. 1.7e-48;

> > Length

505;

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F;180-252/Domain: annexin repeat
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A; Residues: 1-57, 'T', 59-82, 'L', 84-156, 'S', 158-176, 'G', 178-312, 'RY', 315-327 < CHA>
A; Residues: 1-57, 'T', 59-82, 'L', 84-156, 'S', 158-176, 'G', 178-312, 'RY', 315-327 < CHA>
A; Residues: GB: M81844; NID: g178700; PIDN: AAB46383.1; PID: g178701
A; Note: the authors translated the codon TTG for residue 83 as Phe, AGT for residue 157
A; Note: the authors state that the protein sequence differs from that in reference S064
C; Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 10q11.2-10q11.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: 77-Ala, 80-Ala, 96-Ala, 122-Ala were also found R;Chang, K.S.; Wang, G.; Freireich, E.J.; Daly, M.; Naylor, S.L.; Trujillo, J.M.; Stass Blood 79, 1802-1810, 1992
A;Title: Specific expression of the annexin VIII gene in acute promyelocytic leukemia. A;Reference number: A38847; MUID:92216091; PMID:1313714
A;Accession: A38847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: the sequence from Fig. 3 is inconsistent with that in Fig. 1 in lacking 208-Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-327 <HAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eur. J. Biochem. 185, 63-71, 1989
A;Title: Vascular anticoagulant beta: a novel human Ca(2+)/phospholipid binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S06476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Hauptmann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: S06476; A38847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N; Alternate names: vascular anticoagulant beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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        267-283/Region: endonexin
                                                                                                                                                                      96-167/Domain: annexin repeat homology <AX2>;107-123/Region: endonexin fold #status predi
                                                                                                                                                                                                                                                                                                                 Superfamily: annexin I; annexin repeat homology
Keywords: calcium binding; duplication; endonexin fold; phospholipid binding; 2-327/Product: annexin VIII #status predicted <NAT>
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                                                          192-208/Region: endonexin fold #status predicted 256-327/Domain: annexin repeat homology <a href="https://www.enangeriches.com/regions-new-market-besselfer-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-besself-be
                                                                                                                                                                                                                                                                                                        24-95/Domain: annexin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Cross-references: GDB:128069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Gene: GDB:ANX8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: EMBL:X16662
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                                                                                                                                                                                                                                                               5-51/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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J. Biochem. 185, 63-71, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6-Ala was also found
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
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    homology <AX4>
#status predict
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Best Local
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                                                                                                                                                                                                                                                      134 AYEEDYGSSLEEDIQADTSGYLERILVCLLQGSRDDVSSFVDPALALQDAQDLYAAGEKI 193
                                                                                                                                                                                                                                                                                  128 VYESEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDP-DAGIDEAQVEQDAQALFQAGELK 186
                                                                                                                                                                                                                                                                                                                   74 TLKSELSGKFERLIVALMYPPYRYEAKELHDAMKGLGTKEGVIIEILASRTKNQLREIMK 133
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                                                                                                      DYKKALLLCGED 319
                                                                                                                               LHSYFAERLYYAMKGAGTRDGTLIRNIVSRSEIDLNLIKCHFKKMYGKTLSSMIMEDTSG 313
                                                                                                                                                                                          RGTDEMKFITILCTRSATHLLRVFEEYEKIANKSIEDSIKSETHGSLEEAMLTVVKCTQN
                                                                           DYKNALLSLVGSD 326
                                                                                                                                                           IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKBFRKNFATSLYSMIKGDTSG 306
                                                                                                                                                                                                             WGTDEBKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
                                                                                                                                                                                                                                                                                                                                                 DLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQ 127
                                                                                                                                                                                                                                                                                                                                                                               TVKSSSHFNPDPDAETLYKAMKGIGTNEQAIIDVLTKRSNTQRQQIAKSFKAQFGKDLTE
                                                                                                                                                                                                                                                                                                                                                                                                          TVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 832.5; UB 1,
Pred. No. 1.3e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #text_change 22-Jun-1999
C;Accession: A47658; B29250; Ā41213; B31046; A60707
R;Tait, J.F.; Smith, C.; Xu, L.; Cookson, B.T.
Genomics 18, 79-86, 1993
Genomics 18, 79-86, 1993 A;Cross-references: EMBL:M20560; NID:g186967; PIDN:AAA59496.1; PID:g307115; EMBL:J0389 R;Ross, T.S.; Tait, J.F.; Majerus, P.W. Science 248, 605-607, 1990 A;Title: Identity of inositol 1,2-cyclic phosphate 2-phosphohydrolase with lipocortin A;Reference number: A41213; MUID:90239555; PMID:2159184 J. Biol. Chem. 263, 10799-10811, 1988
A;Title: Five distinct calcium and phospholipid binding proteins share homology with lip
A;Reference number: A92659; MUID:88273202; PMID:2968983 A;Cross-references: GB:L20591; NID:g410200; PIDN:AAAA16713.1; PID:g410202 R;Pepinsky, R.B.; Tizard, R.; Mattaliano, R.J.; Sinclair, L.K.; Miller, J. Biol. Chem. 263, 10799-10811. 1988 A; Molecule type: mRNA A; Residues: 1-323 < PEP> A; Title: Structure and polymorphisms of the human annexin III (ANX3) A; Reference number: A47658; MUID:94102764; PMID:8276419 N;Alternate names: 1,2-cyclic-inositol-phosphate phosphodiesterase A;Accession: B29250 A; Residues: 1-323 < RES> A; Molecule type: DNA A; Status: translation not shown A; Accession: A47658 PIDN:AAA59496.1; PID:g307115; EMBL:J03899 (EC 3.1.4.36); G.T.; Browning,

A;Residues: 41-79;85-88;104-119;126-128,'X',130-145,'G',147-153,'X',155-157,'X',159-160; R;Ernst, J.D.; Hoye, E.; Blackwood, R.A.; Jaye, D. J. Clin. Invest. 85, 1065-1071, 1990

A; Title: Placental anticoagulant proteins: isolation and A; Reference number: A90534; MUID:89118212; PMID:2975506

comparative

characterization

A; Molecule type: protein A; Accession: B31046 A;Molecule type: protein A;Residues: 41-102;126-138 <ROS> A;Residues: 41-102;126-138 <ROS> B;Tait, J.F.; Sakata, M.; McMullen, B.A.; Miao, C.H.; Funakoshi, T.; Hendrickson, L.E.; Biochemistry 27, 6268-6276, 1988

A;Accession: A41213

A; Title: Purification and characterization of an abundant cytosolic protein A; Reference number: A60707; MUID:90203211; PMID:2138632

from

human

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A;Molecule type: protein
A;Residues: 42-55;74-82;105-126;155-169;177-204,'L',206-209;264-274;305-315 <ERN>
C;Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 4g21-4g21
A; Introns: 5/3; 35/1; 66/3; 104/3; 135/1; 161/3; 180/3; 212/1; 244/1; 263/3; 304/3
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                                                                                                                                                                                                                                                                                                                                          N;Alternate names: 1,2-cyclic-inositol-phosphate phosphodiesterase (EC 3.1.4.36);
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 07-Oct-1994
C;Accession: A29250
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A;Title: Five distinct calcium and phospholipid binding proteins share homology with liphy. Reference number: A92659; MUID:88273202; PMID:2968983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                    C;Superfamily: annexin I; annexin repeat homology C;Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid bi F;2-324/Product: annexin III #status predicted <MAT>
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;188-204/Region: endonexin fold #status predicted
;252-323/Domain: annexin repeat homology <AX4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .93-164/Domain: annexin repeat homology <AX2>,104-120/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid;2-323/product: annexin III #status predicted <MAT>
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                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-324 < PEP>
                                                                                                                                     A,Cross-references: GB:M20559; GB:J03898
C,Comment: Annexins undergo reversible,
                                                                                                                                                                                                                                  A;Accession: A29250
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252-323/Domain: annexin repeat
263-279/Region: endonexin fold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-92/Domain: annexin repeat homology <AX1>
32-48/Region: endonexin fold #status predicted
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                     22-93/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTPAFLAERLHRALKGIGTDEFTLNRIMVSRSEIDLLDIRTEFKKHYGYSLYSAIKSDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RWGTDEDKFTEILCLRSFPQLKLTFDEYRNISQKDIVDSIKGELSGHFEDLLLAIVNCVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQAYYTVYKKSIGDDISSETSGDFRKALLTLADGRRDESLKVDEHLAKQDAQILYKAĞEN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KÓAÅEBEÁGSSÍFBDAAAGDÍZSGAAAWTAATTÖVNADABOBOROTÓBYÓYTEÓYGET 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGTVRDYPDFSPSVDAEAIQKAIRGIGTDEKMLISILTERSNAQRQLIVKEYQAAYGKEL
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annexin repeat endonexin fold
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#status predicted
                          homology <AX1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #status predicted (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 811; DB 1
Pred. No. 3e-45;
1; Mismatches
                                                                                                                                               calcium-dependent binding to membrane
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F;94-165/Domain: annexin repeat homology <AX2>
F;105-121/Region: endonexin fold #status predicted
F;177-249/Domain: annexin repeat homology <AX3>
F;189-205/Region: endonexin fold #status predicted
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C;Date: 30-Sep-1992 #sequence_revision 26-Jan-1996 #text_change 22-Jun-1 C;Accession: A54467; A32554; A39513; B39513
C;Accession: A54467; A32554; A39513; B39513
C;Accession: A54467; A32554; A39513; B39513
C;Accession: A54467; A32554; A39513; B39513
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A;Title: Calcium channel activity of purified human synexin and A;Reference number: A32554; MUID:89264510; PMID:2542947,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Divergent structure of the human synexin (annexin A;Reference number: A54467; MUID:94264005; PMID:7515686 A;Accession: A54467
                                                                                                                                        A;Cross-references: EMBL:J04543; NID:g338243; PIDN:AAA36616.1; PID:g338; R;Magendzo, K.; Shirvan, A.; Cultraro, C.; Srivastava, M.; Pollard, H.B. J. Biol. Chem. 266, 3228-323, 1991
A;Title: Alternative splicing of human synexin mRNA in brain, cardiac, A;Reference number: A39513; MUID:91131630; PMID:1825209
A;Accession: A39513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: synexin
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A; Residues: 1-145,168-488 <BUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 33, 6888-6901, 1994
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;20,219/Binding:
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                                                                      A; Molecule type: mRNA
A; Residues: 137-145, 168-176 < MAG>
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Best Local 9
A;Accession: B395
                                   A; Cross-references: EMBL:J05732
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pred. No. 1.5e-43;
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A; Molecule type: mkNA A; Residues: 137-176 < MA2>

mRNA

Annexins undergo

reversible,

calcium-dependent

binding

6

ae

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A;Molecule type. - ZHF>
A;Residues: 1-463 <ZHF>
R;Zhang-Keck, Z.Y.; Burns, A.L.; Pollard, H.B.
                                                                                                                           A;Cross-references: EMBL:L13129
R;Zhang-Keck, Z.Y.; Srivastava, M.; Kozak, C.A.; Caohuy, H.; Shirvan, Biochem. J. 301, 835-845, 1994
A;Title: Genomic organization and chromosomal localization of the mous A;Reference number: S46209; MUID:94330961; PMID:8053909
                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence revision 01-Sep-1995 #text_change 13-Aug-1999
C;Accession: S29170; S46209; $\overline{5}\)51173
R;Zhang-Keck, Z:Y; Burns, A.L.; Pollard, H.B.
Biochem. J. 289, 735-741, 1993
A;Title: Mouse synexin (annexin VII) polymorphisms and a phylogenetic comparison with A;Reference number: S29170; MUID:93168121; PMID:7916616
A;Accession: S29170
                                                                                              A; Accession: S46209
A; Molecule type: DN
                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-463 < ZHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N; Alternate names: synexin
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F;1-45,168-488/Product: annexin VII, short form #status predicted <MA3>
F;188-259/Domain: annexin repeat homology <AX1>
F;199-215/Region: endonexin fold #status predicted
F;260-331/Domain: annexin repeat homology <AX2>
F;771-287/Region: endonexin fold #status predicted
F;343-415/Domain: annexin repeat homology <AX3>
F;371-287/Region: endonexin fold #status predicted
F;343-415/Domain: annexin repeat homology <AX3>
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A;Introns: 17/3; 87/1; 124/1; 145/3; 167/3; 202/2; 233/3; 271/3; 328/3; 385/3; 411/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: annexin VII; annexin repeat homology C;Keywords: alternative splicing; calcium binding; calcium channel; duplication; endones
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Best Local Similarity
Matches 153; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQCALNRPAFFAERLYYAMKGAGTDDSTLVRIVVTRSEIDLVQIKQMPAQMYQKTLGTMI
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Pred. No. 5.1e-43;
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C;Superfamily: annexin I; annexin repeat homology C;Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid bin F;2-316/Product: annexin IV #status experimental <MAT>
F;88.159/Domain: annexin repeat homology <AX2>
F;99-115/Region: endonexin fold #status predict
F;171-243/Domain: annexin repeat homology <AX3:
                                                                              F;16-87/Domain: annexin repeat homology <AX1>F;27-43/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 2-9,'D',11-30;246-251,'E'
C;Coment: Annexins undergo reversible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Schlaepfer, D.D.; Fisher, D.A.; Brandt, M.E.; Bode, H.R.; Jones, J.M.; Haigler, H.T. J. Biol. Chem. 267, 9529-9539, 1992
A;Title: Identification of a novel annexin in Hydra vulgaris. Characterization, cDNA clo A;Reference number: A42660; MUID:92250599; PMID:1339458
                                                                                                                                                                                                                                                                                                      derstood
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A; Residues: 1-316 < SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Hydra vulgaris
C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 22-Jun-1999
C;Accession: A42660; B42660
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F;235-306/Domain: annexin repeat homology <aX2>
F;318-390/Domain: annexin repeat homology <aX3>
F;318-394-467/Domain: annexin repeat homology <ax3>
F;318-344-467/Domain: annexin 
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A;Residues: 1-144,'8',146-303,'A',305-463 <ZHW>
A;Cross-references: EMBL:L13129; NID:g293293; PIDN:AAA37238.1; PID:g293294
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A;Accession. ceiin
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C;Date: 28-Dec-1987 #sequence revision 30-Sep-1992 #text_change 16-Jun-2000
C;Date: 28-Dec-1987 #sequence Perision 30-Sep-1992 #text_change 16-Jun-2000
C;Accession: A23942; JH0305; Ā45440; PC2039; C53507; A23717; A05153
R;Huang, K.S.; Wallner, B.P.; Mattaliano, R.J.; Tizard, R.; Burne, C.; Frey
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell 46, 191-199, 1986
A;Title: Two human 35 kd inhibitors of phospholipase A2
A;Reference number: A90881; MUID:86245065; PMID:3013422
A;Accession: A23942
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                                                                                                                                                           A;Cross-references: DDBJ:D00017; NID:g219909; PIDN:BAA00013.1; R;Emans, N.; Gorvel, J.P.; Walter, C.; Gerke, V.; Kellner, R.; J. Cell Biol. 120, 1357-1369, 1993
                                                                                                                                                                                                                                                   A;Title: Characterization of the human lipocortin-2-encoding A;Reference number: JH0305; MUID:91065537; PMID:2174397 A;Accession: JH0305
                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:D00017; GB:M14043; NID:g219909; PIDN:BAA00013.1;
                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
                                              A;Molecule type: protein
A;Residues: 234-241;252-261 <EMA>
A;Note: this protein was demonstrated in early endosomes
                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-339 <SPA>
                                                                                                         A; Accession: A45440
                                                                                                                        A; Title: Annexin II is a major component of fusogenic e. A; Reference number: A45440; MUID:93194942; PMID:8449982
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.;Wright, J.F.; Kurosky, A.; Wasi, S.
Liochem. Biophys. Res. Commun. 198, 983-989,
.;Title: An endothelial cell-surface form of
                                                                                                                                                                                                                                                                                                                                                                                                   Residues: 1-339 <HUA>
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A; No. 100 type: protein A; Molecule type: protein A; Residues: 18-37;119-126;172-191;301-304, 'X', 306-307 R: Hvatt, S.L.; Liao, L.; Chapline, C.; Jaken, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Comment: Annexins undergo reversible, calcium-dependent binding to C;Comment: Calpactin I, a tetramer of two heavy chains and two light oskeleton and be involved with exocytosis.
C;Comment: Annexin II is the heavy chain component of calpactin I. The C;Comment: Annexin II is the heavy chain component of calpactin I. These ligation is two moles of calcium ion per mole of annexin II. These ligations is the heavy chain component of calpactin I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 266, 5169-5176, 1991
A;Title: The protein-tyrosine kinase substrate, calpactin A;Reference number: A23717; MUID:91161611; PMID:1825830
A;Accession: A23717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;ACCEPTION A;ACCEPTION A;ACCEPTION A;ACCEPTION A;Molecule type: protein A;Rolecule type: protein A;Residues: 'LXXXX',15-28,'p',30-40;50-51,'XX',54-63 A;Residues: 'LXXXXX',15-28,'p',30-40;50-51,'XX',54-63 A;Residues: 'LXXXX',15-28,'p',30-40;50-51,'XX',54-63 A;Residues: 'LXXXXX',15-28,'p',30-40;50-51,'XX',54-63 A;Residues: 'LXXXXX',15-28,'p',30-40;50-51,'XX',54-63 A;Residues: 'LXXXXX',15-28,'p',30-40;50-51,'XX',54-63 A;Residues: 'LXXXX',15-28,'p',30-40;50-51,'XX',15-63 A;Residues: 'LXXXX',15-28,'p',30-40;50-51,'XX',15-63 A;Residues: 'LXXXX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40;50-51,'XX',15-28,'p',30-40,'p',30-40,'p',30-40,'p',30-40,'p',30-40,'p',30-40,'p',30-40,'p',30-40,'p',30-40,'p',30-40,'p',30-40,'p',30-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Hyatt, S.L.; L
Biochemistry 33,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 15q21-15q22
A;Introns: 16/3; 50/1; 81/3; 119/3; 150/1; 176/3; 196/3; 228/1; 260/1; 27
C;Superfamily: annexin I; annexin repeat homology
C;Keywords: acetylated amino end; actin binding; calcium binding; duplica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: C53507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 11-28; 50-63; 69-77; 120-135; 314-324; 330-339 < JIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;268-339/Domain: annexin repeat homology <AX4>
F;279-295/Region: endonexin fold #status predicted
F;2/Modified site: acetylated amino end (Ser) (in mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;192-264/Domain: annexin repeat homology <AX3>F;204-220/Region: endonexin fold #status predicted
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                                                                                                                                                                                                                                                                                                                                205
                                                                                                                                                                                                                                                                                                                                                                                                    186 KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 QVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDEDAG-IDEAQVEQDAQALFQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146;
325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA
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                                                                                                                                                                                                                                   SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGD
                                                                                                                                                            NKPLYFÄDRLYDSMKGKGTRDKVLIRIMVSRSEVDMLKIRSEFKRKYGKSLYYYIQQD
    GDYQKALLYLCGGDD
                                                                                GDYKKALLLLCGEDD 320
                                                                                                                                                                                                                                                                                                                                RKĠTĎVPKWÍSIMTERSVPHĽQKVFĎRYKSYSPYDMLÉSÍRKEVKGDĽÈNAFĽNLVQC
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phosphate (Ser)
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46.3%; Pred. No. 1.3e-38;
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        339
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R.G.;
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C;Superfamily: annexin repeat homology F;373-444/Domain: annexin repeat homol
                                     F;445-516/Domain:
                                                                                      C; Genetics:
A; Introns: 69/3; 161/1; 208/3;
                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-676 <BER>
                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                               A; Reference number: A; Accession: S41022
                                                                                                                                                                                                                 submitted to the EMBL Data A; Reference number: S41014
                                                                                                                                                                                                                                                        R;Berks,
                                                                                                                                                                                                                                                                                                         hypothetical protein T07C4.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. J. 316, 729-735, 1996
A;Title: Novel isoforms of synexin in Xenopus laevis: multiple tandem
A;Reference number: S70644; MUID:96265035; PMID:8670145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Xenopus laevis (African clawed frog)
C;Date: 14-Feb-1997 #sequence revision 13-Mar-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annexin VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;Residues: 1-512 <SRI>
                     528-600/Domain:
                                                                                                                   Cross-references: EMBL:Z29443; NID:g1067051; PID:g443836
                                                                                                                                                                                                                                                                       Accession: S41022
                                                                                                                                                                                                                                                                                         ;Date: 06-Jan-1995
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;Srivastava, M.; Z)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Date: 14-Feb-1997 #sequence_revision
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                  499
                                                                                                                                                                                                                                                                                                                                                                                                                                                    305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 RSIPAYLAETLYYAMKGAGTDDHTLIRVMVSBSEIDLENIRKEFRKNFATSLYSMIKGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 LKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319 VACYKQEFGREIEKDIRSDTSGHFERLLISIMARGIVDESQNVNMQQAEQDAQRLYQAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 KQVYEEEYGSSLEDDVVGDTSGYYQRMLV-VLLQANRDPDAGIDEAQVEQDAQALFQAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148;
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                                                                                                                                                                                                                                                                                                                                                                                                                SGAYKRMLLAISG 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKLGTDESSFNLVLASRSFPQLKAVAEAYARISKRDLLSVIGREFSGYIEDGLKAVLQCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKDLKŚELSGNVĖELITALFMPSTYYDAWSLYNAMKGAGTQERVLIBILCTKTNSEIRNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGTIKAAPNFDALSDAEKLRKAMKGFGTDEKPI-DVVANRSNDQRQKIQAAFKTAYGKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
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annexin repeat
                annexin repeat
                                    annexin repeat
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                                                                                                                                                                                                                                                                                  #sequence_revision
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                                                                                    227/1; 357/1; 505/3
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homology
                  homology
                                homology
                                                    homology <AX1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 706; DB 2;
Pred. No. 3.2e-38;
                                                                                                                                                                                                                                 January
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                                                                                                                                                                                                                                                                            06-Jan-1995 #text_change 09-Sep-1997
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<AX4>
                  <AX3>
                                     <AX6>
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                                                                                                                                                                                                                                 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID:g790544
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                           302
                                                                                242
                                                                                                              537
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                                                     597 AVIRNRPAYFAKLIHDSMKGLGTRDNDL
                                                                                                                                        182
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                                                                                                                                                                                                                            417
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                                                                                                                                                                                                                                                                                                                                         146;
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                                                                            KSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMYSRSEIDLFNIRKEFRKNFATSLYSMIK 301
                                                                                                                                                               IQQVRDAYKMLFKKDLERDLIGETSGHFKRLLVSLCAGGRDESSQTDGLRANQDARRLLQ
                                                                                                                                                                                          LRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQ
                                                                                                                                                                                                                       GKDLIKELKGELHGDFEDLILALMDAPAIYDAKQLHRAMEGLGTKESVLIEIMTSRTNAQ 476
                                                                                                                                                                                                                                                GRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 121
                                                                                                                                                                                                                                                                                                        VLRGTVTDFP--GFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLF 61
                                                                                                                                  AGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVV 241
                                                                                                                                                                                                                                                                               VMIGTPSVFPVQGFNSNADAEVLRKANKGLGCNNSKVISILCQRTNWQRQEISKAFKVMY 416
                         GDTSGDYKKALLLL
                                                                                                          AGEKRLGTDESTFNAILASQNFSQLRLVFEEYQKASNHSIEKAIEFEFSGDIRDGLLAVI
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                     44.1%;
670
                         315
                                                                                                                                                                                                                                                                                                                                         63;
                                                                                                                                                                                                                                                                                                                                                   Score 706; DB 2;
Pred. No. 4.5e-38;
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                                                                                                                                                                                                                                                                                                                                                               Length 676
                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                  536
                                                  656
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annexin II -LUBO36 bovine

N;Alternate names: 36K protein; calcium-dependent phospholipid-actin-binding C;Species: Bos primigenius taurus (cattle) C;Date: 04-Dec-1986 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999 C;Date: 04-Dec. ACCESSION: A03081; S02477 protein; ca

Accession: A03081; S02477

R;Kristensen, T.; Saris, C.J.M.; Hunter, T.; Biochemistry 25, 4497-4503, 1986 A;Title: Primary structure of bovine calpact: calpactin I Hicks, L.J.; Noonan, D.J.; Glenney Jr., heavy chain (p36), a major cellular sub J.R

A;Reference number: A03081; MUID:87026517; PMID:2945590 A;Accession: A03081

A; Molecule type: mRNA

A;Residues: 1-339 <KRI>

R;Martin, A;Cross-references: GB:M14056; NID:g162778; PIDN:AAA30421.1; PID:g162779
A;Experimental source: Madin-Darby kidney cell line MDBK F.; Derancourt, J.; Capony, J.P.; Watrin, J. 251, 777-785, 1988 A.; Cavadore, J.C.

n-severing properties. A; Title: A 36 kDa monomeric S02477; MUID:88326216; PMID:2970844 protein and its complex with a 10 kDa protein both isolated

A;Reference number: A;Accession: S02477

A;Molecule type: protein A;Residues: 27-61 <MAR> A;Experimental source: aorta

A;Note: 44-Lys was also found R;Glenny Jr., J.R.; Boudreau, M.; Galyean, R.; Hunter, J. Biol. Chem. 261, 10485-10488, 1986 T.; Tack,

NH2-terminal

A;Title: Association of the S-100-related calpactin I light chain with the A;Reference number: A38844; MUID:86278112; PMID:2942542 A;Contents: annotation, amino-terminal acetylation

derstood Comment: Annexins undergo reversible, calcium-dependent binding to membrane 18 phospholip found in

C;Comment: Calpactin I, a tetramer of two heavy chains and two light chains, oskeleton and be involved with exocytosis.

C;Comment: Annexin II is the heavy chain component of calpactin I. The affinity of annex I I binds two moles of calcium ion per mole of annexin II. These ligands make annexin II C;Comment: Annexin II annexin I as a regulator of intracellular phospholipase activity. C;Superfamily: annexin I; annexin repeat homology C;Keywords: acetylated amino end; actin binding; calcium binding; duplication; endonexin F;2-339/Product: annexin II #status experimental <MAT>
F;2-12/Region: calpactin I light chain binding #status predicted
F;36-107/Domain: annexin repeat homology <AX1>

1. 18 36.30

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F;47-63/Region: endonexin fold #status predicted
F;108-179/Domain: annexin repeat homology <AX2>
F;119-135/Region: endonexin fold #status predicted
F;119-264/Domain: annexin repeat homology <AX3>
F;192-264/Domain: annexin fold #status predicted
F;204-220/Region: endonexin fold #status predicted
F;268-339/Domain: annexin repeat homology <AX4>
F;279-295/Region: endonexin fold #status predicted
F;27/Nodified site: acetylated amino end (Ser) (in mature form) #status experimental
F;24/Binding site: phosphate (Tyr) (covalent) #status predicted
F;24/Binding site: phosphate (Ser) (covalent) #status predicted
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                                                                                                                                                                                               186 KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 245
                                                                                                                                                                                                                                                               205 RKGTDVPKWISIMTERSVCHLOKVPERYKSYSPYDMLESIKKEVKGDLENAFLNLVQCIQ 264
                                                                                                                                                                                                                                                                                                             127
265 NKPLYFADRLYDSMKGKGTRDKVLIRIMVSRSEVDMLKIRSEFKKKYGKSLYYYIQQDTK 324
                                                                                                              246 SIPAYLABTLYYAMKGAGTDDHTLIRVMYSRSEIDLFNIRKEFRKUFATSLYSMIKGDTS 305
                                                                                                                                                                                                                                                                                                                                                     85 SALKSALSGHLETVILGLLKTPAQYDASELKASMKGLGTDEDSLIEIICSRTNQELQEIN 144
                                                                                                                                                                                                                                                                                                                                                                                            67 DDĻĶSEĻTĢKFĒKLĮVAĻMĶPSRLYDĀYĒĻĶHĀLĶĢĀĢTNĒKVĻTĒJĪĀSRTPĒĒĻRĀĮK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                      7 GTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLL
                                                                                                                                                                                                                                                                                                  QVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAG-IDEAQVEQDAQALFQAGEL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 339;
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